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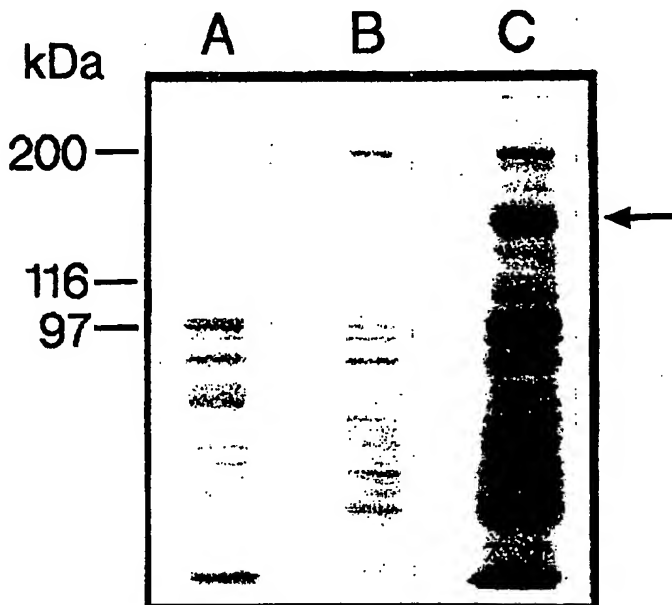
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(57) Abstract

A recombinant or isolated integrin heterodimer comprising a novel subunit $\alpha 10$ in association with a subunit β is described. The $\alpha 10$ integrin may be purified from bovine chondrocytes on a collagen-type-II affinity column. The integrin or the subunit $\alpha 10$ can be used as marker or target of all types of cells, e.g. of chondrocytes, osteoblasts and fibroblasts. The integrin or subunit $\alpha 10$ thereof can be used as marker or target in different physiological or therapeutic methods. They can also be used as active ingredients in pharmaceutical compositions and vaccines.



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AN INTEGRIN HETERODIMER AND A SUBUNIT THEREOF

FIELD OF THE INVENTION

The present invention relates to a recombinant or isolated integrin heterodimer comprising a subunit $\alpha 10$.
5 and a subunit β , the subunit $\alpha 10$ thereof, homologues and fragments of said integrin and of said subunit $\alpha 10$ having similar biological activity, processes of producing the same, polynucleotides and oligonucleotides encoding the same, vectors and cells comprising the same, binding
10 entities binding specifically to the same, and the use of the same.

BACKGROUND OF THE INVENTION

The integrins are a large family of transmembrane
15 glycoproteins that mediate cell-cell and cell-matrix interactions (1-5). All known members of this superfamily are non-covalently associated heterodimers composed of an α - and a β -subunit. At present, 8 β -subunits ($\beta 1$ - $\beta 8$) (6) and 16 α -subunits ($\alpha 1$ - $\alpha 9$, αv , αM , αL , αX , αIIb , αE and
20 αD) have been characterized (6-21), and these subunits associate to generate more than 20 different integrins. The $\beta 1$ -subunit has been shown to associate with ten different α -subunits, $\alpha 1$ - $\alpha 9$ and αv , and to mediate interactions with extracellular matrix proteins such as colla-
25 gens, laminins and fibronectin. The major collagen binding integrins are $\alpha 1\beta 1$ and $\alpha 2\beta 1$ (22-25). The integrins $\alpha 3\beta 1$ and $\alpha 9\beta 1$ have also been reported to interact with collagen (26,27) although this interaction is not well understood (28). The extracellular N-terminal regions of
30 the α and β integrin subunits are important in the binding of ligands (29,30). The N-terminal region of the α -subunits is composed of a seven-fold repeated sequence (12,31) containing FG and GAP consensus sequences. The repeats are predicted to fold into a β -propeller domain

(32) with the last three or four repeats containing putative divalent cation binding sites. The α -integrin subunits $\alpha 1$, $\alpha 2$, αD , αE , αL , αM and αX contain a ~200 amino acid inserted domain, the I-domain (A-domain), which
5 shows similarity to sequences in von Willebrand factor, cartilage matrix protein and complement factors C2 and B (33,34). The I-domain is localized between the second and third FG-GAP repeats; it contains a metal ion-dependent
10 adhesion site (MIDAS) and it is involved in binding of ligands (35-38).

Chondrocytes, the only type of cells in cartilage, express a number of different integrins including $\alpha 1\beta 1$, $\alpha 2\beta 1$, $\alpha 3\beta 1$, $\alpha 5\beta 1$, $\alpha 6\beta 1$, $\alpha v\beta 3$, and $\alpha v\beta 5$ (39-41). It has been shown that $\alpha 1\beta 1$ and $\alpha 2\beta 1$ mediate chondrocyte inter-
15 actions with collagen type II (25) which is one of the major components in cartilage. It has also been shown that $\alpha 2\beta 1$ is a receptor for the cartilage matrix protein chondroadherin (42).

20 SUMMARY OF THE INVENTION

The present invention relates to a novel collagen type II binding integrin, comprising a subunit $\alpha 10$ in association with a subunit β , especially subunit $\beta 1$, but also other β -subunits may be contemplated. In preferred
25 embodiments, this integrin has been isolated from human or bovine articular chondrocytes, and human chondrosarcoma cells.

The invention also encompasses integrin homologues of said integrin, isolated from other species, such as
30 bovine integrin heterodimer comprising a subunit $\alpha 10$ in association with a subunit β , preferably $\beta 1$, as well as homologues isolated from other types of human cells or from cells originating from other species.

The present invention relates in particular to a
35 recombinant or isolated integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, and homologues and or fragments thereof having the

same biological activity.

The invention further relates to a process of producing a recombinant integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID

5 No. 2, or homologues or fragments thereof having similar biological activity, which process comprises the steps of

a) isolating a polynucleotide comprising a nucleotide sequence coding for a integrin subunit $\alpha 10$, or homologues or fragments thereof having similar biological
10 activity,

b) constructing an expression vector comprising the isolated polynucleotide,

c) transforming a host cell with said expression vector,

15 d) culturing said transformed host cell in a culture medium under conditions suitable for expression of integrin subunit $\alpha 10$, or homologues or fragments thereof having similar biological activity, in said transformed host cell, and, optionally,

20 e) isolating the integrin subunit $\alpha 10$, or homologues or fragments thereof having the same biological activity, from said transformed host cell or said culture medium.

The integrin subunit $\alpha 10$, or homologues or fragments thereof having the same biological activity, can also be
25 provided by isolation from a cell in which they are naturally present.

The invention also relates to an isolated polynucleotide comprising a nucleotide coding for a integrin subunit $\alpha 10$, or homologues or fragments thereof having
30 similar biological activity, which polynucleotide comprises the nucleotide sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or parts thereof.

The invention further relates to an isolated polynucleotide or oligonucleotide which hybridises to a DNA
35 or RNA encoding an integrin subunit $\alpha 10$, having the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or homologues or fragments thereof, wherein said polyoligo-

nucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding the integrin subunit $\alpha 1$.

The invention relates in a further aspect to vectors comprising the above polynucleotides, and to cells containing said vectors and cells that have polynucleotides or oligonucleotides as shown in SEQ ID No. 1 or 2 integrated in their genome.

The invention also relates to binding entities having the capability of binding specifically to the integrin subunit $\alpha 10$ or to homologues or fragments thereof, such as proteins, peptides, carbohydrates, lipids, natural ligands, polyclonal antibodies or monoclonal antibodies.

In a further aspect, the invention relates to a recombinant or isolated integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , in which the subunit $\alpha 10$ comprises the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or homologues or fragments thereof having similar biological activity.

In a preferred embodiment thereof, the subunit β is $\beta 1$.

The invention also relates to a process of producing a recombinant integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , in which the subunit $\alpha 10$ comprises the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, which process comprises the steps of

a) isolating one polynucleotide comprising a nucleotide sequence coding for a subunit $\alpha 10$ of an integrin heterodimer and, optionally, another polynucleotide comprising a nucleotide sequence coding for a subunit β of an integrin heterodimer, or for homologues or fragments thereof having similar biological activity,

b) constructing an expression vector comprising said isolated polynucleotide coding for said subunit $\alpha 10$ in combination with an expression vector comprising said isolated nucleotide coding for said subunit β ,

c) transforming a host cell with said expression vectors,

d) culturing said transformed host cell in a culture medium under conditions suitable for expression of an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or homologues or fragments thereof similar biological activity, in said transformed host cell, and, optionally,

e) isolating the integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or homologues or fragments thereof having the same biological activity, from said transformed host cell or said culture medium.

The integrin heterodimer, or homologues or fragments thereof having similar biological activity, can also be provided by isolation from a cell in which they are naturally present.

The invention further relates to a cell containing a first vector, said first vector comprising a polynucleotide coding for a subunit $\alpha 10$ of an integrin heterodimer, or for homologues or parts thereof having similar biological activity, which polynucleotide comprises the nucleotide sequence shown in SEQ ID No. 1 or SEQ ID No. 2 or parts thereof, and, optionally, a second vector, said second vector comprising a polynucleotide coding for a subunit β of an integrin heterodimer, or for homologues or fragments thereof.

In still another aspect, the invention relates to binding entities having the capability of binding specifically to the integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or to homologues or fragments thereof having similar biological activity, preferably wherein the subunit β is $\beta 1$. Preferred binding entities are proteins, peptides, carbohydrates, lipids, natural ligands, polyclonal antibodies and monoclonal antibodies.

In a further aspect, the invention relates to a fragment of the integrin subunit $\alpha 10$, which fragment is a peptide chosen from the group comprising peptides of

the cytoplasmic domain, the I-domain and the spliced domain.

In one embodiment, said fragment is a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ.

5 In another embodiment, said fragment comprises the amino acid sequence from about amino acid no. 952 to about amino acid no. 986 of SEQ ID No. 1.

In a further embodiment, said fragment comprises the amino acid sequence from about amino acid No. 140
10 to about amino acid No. 337 in SEQ ID No. 1.

Another embodiment of the invention relates to a polynucleotide or oligonucleotide coding for a fragment of the human integrin subunit $\alpha 10$. In one embodiment this polynucleotide of oligonucleotide codes for a fragment
15 which is a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain. In further embodiments the polynucleotide or oligonucleotide codes for the fragments defined above.

The invention also relates to binding entities having the capability of binding specifically to a fragment
20 of the integrin subunit $\alpha 10$ as defined above.

The invention also relates to a process of using an integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or an integrin
25 heterodimer comprising said subunit $\alpha 10$ and a subunit β , or a homologue or fragment of said integrin or subunit having similar biological activity, as a marker or target molecule of cells or tissues expressing said integrin subunit $\alpha 10$, which cells or tissues are of animal including human origin.
30

In an embodiment of this process the fragment is a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain.

In further embodiments of said process the fragment
35 is a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ, or a fragment comprising the amino acid sequence from about amino acid No. 952 to

about amino acid No. 986 of SEQ ID No. 1, or a fragment comprising the amino acid sequence from about amino acid no. 140 to about amino acid no. 337 of SEQ ID no. 1.

5 The subunit β is preferably $\beta 1$. The cells are preferably chosen from the group comprising chondrocytes, smooth muscle cells, endothelial cells, osteoblasts and fibroblasts.

Said process may be used during pathological conditions involving said subunit $\alpha 10$, such as pathological
10 conditions comprising damage of cartilage, or comprising trauma, rheumatoid arthritis and osteoarthritis.

Said process may be used for detecting the formation of cartilage during embryonal development, or for detecting physiological or therapeutic reparation of cartilage.

15 Said process may also be used for selection and analysis, or for sorting, isolating or purification of chondrocytes.

A further embodiment of said process is a process for detecting regeneration of cartilage or chondrocytes
20 during transplantation of cartilage or chondrocytes.

A still further embodiment of said process is a process for in vitro studies of differentiation of chondrocytes.

The invention also comprises a process of using
25 binding entities having the capability of binding specifically to an integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or an integrin heterodimer comprising said subunit $\alpha 10$ and a subunit β , or to homologues or fragments thereof having
30 similar biological activity, as markers or target molecules of cells or tissues expressing said integrin subunit $\alpha 10$, which cells or tissues are of animal including human origin.

The fragment in said process may be a peptide chosen
35 from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain. In preferred embodiments said fragment is a peptide comprising the

amino acid sequence KLGFFAHKKIPEEEKREEKLEQ, or a fragment comprising the amino acid sequence from about amino acid No. 952 to about amino acid No. 986 of SEQ ID No. 1, or a fragment comprising the amino acid sequence from about amino acid No. 140 to about amino acid no. 337 of SEQ ID No. 1.

The process may also be used for detecting the presence of an integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or of an integrin heterodimer comprising said subunit $\alpha 10$ and a subunit β , or of homologues or fragments thereof having similar biological activity.

In a further embodiment said process is a process for determining the differentiation-state of cells during embryonic development, angiogenesis, or development of cancer.

In a still further embodiment this process is a process for detecting the presence of an integrin subunit $\alpha 10$, or of a homologue or fragment of said integrin subunit having similar biological activity, on cells, whereby a polynucleotide or oligonucleotide chosen from the group comprising a polynucleotide or oligonucleotide chosen from the nucleotide sequence shown in SEQ ID No. 1 is used as a marker under hybridisation conditions wherein said polynucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$. Said cells may be chosen from the group comprising chondrocytes, smooth muscle cells, endothelial cells, osteoblasts and fibroblasts. Said integrin fragment may be a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain, such as a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ, or a fragment comprising the amino acid sequence from about amino acid no. 952 to about amino acid no. 986 of SEQ ID No. 1, or a fragment comprising the amino acid sequence from about amino acid No. 140 to about amino acid no. 337 of SEQ ID No. 1.

In a still further embodiment the process is a process for determining the differentiation-state of cells during development, in pathological conditions, in tissue regeneration or in therapeutic and physiological reparation of cartilage. The pathological conditions may be any pathological conditions involving the integrin subunit $\alpha 10$, such as rheumatoid arthritis, osteoarthritis or cancer. The cells may be chosen from the group comprising chondrocytes, smooth muscle cells, endothelial cells, osteoblasts and fibroblasts.

The invention also relates to a process for determining the differentiation-state of cells during development, in pathological conditions, in tissue regeneration and in therapeutic and physiological reparation of cartilage, whereby a polynucleotide or oligonucleotide chosen from the nucleotide sequence shown in SEQ ID No. 1 is used as a marker under hybridisation conditions wherein said polynucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$. Embodiments of this aspect comprise a process, whereby said polynucleotide or oligonucleotide is a polynucleotide or oligonucleotide coding for a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain, such as a polynucleotide or oligonucleotide coding for a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ, or comprising the amino acid sequence from about amino acid No. 952 to about amino acid no. 986 of SEQ ID No. 1, or the amino acid sequence from about amino acid No. 140 to about amino acid No. 337 of SEQ ID No. 1. Said pathological conditions may be any pathological conditions involving the integrin subunit $\alpha 10$, such as rheumatoid arthritis, osteoarthritis or cancer, or atherosclerosis or inflammation. Said cells may be chosen from the group comprising chondrocytes, smooth muscle cells, endothelial cells, osteoblasts and fibroblasts.

In a further aspect the invention relates to a pharmaceutical composition comprising as an active ingredient a pharmaceutical agent or an antibody which is capable of using an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity, as a target molecule. An embodiment of said pharmaceutical composition is intended for use in stimulating, inhibiting or blocking the formation of cartilage, bone or blood vessels. A further embodiment comprises a pharmaceutical composition for use in preventing adhesion between tendon/ligaments and the surrounding tissue after infection, inflammation and after surgical intervention where adhesion impairs the function of the tissue.

The invention is also related to a vaccine comprising as an active ingredient an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$, or DNA or RNA coding for said integrin subunit $\alpha 10$.

A further aspect of the invention is related to the use of the integrin subunit $\alpha 10$ as defined above as a marker or target in transplantation of cartilage or chondrocytes.

A still further aspect of the invention is related to a method of using binding entities having the capability of binding specifically to an integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or an integrin heterodimer comprising said subunit $\alpha 10$ and a subunit β , or to homologues or fragments thereof having similar biological activity, for promoting adhesion of chondrocytes and/or osteoblasts to surfaces of implants to stimulate osseointegration.

The invention is also related to the use of an integrin subunit $\alpha 10$ or an integrin heterodimer comprising said subunit $\alpha 10$ and a subunit β as a target for anti-

adhesive drugs or molecules in tendon, ligament, skeletal muscle or other tissues where adhesion impairs the function of the tissue.

The invention also relates to a method of stimulating, inhibiting or blocking the formation of cartilage or bone, comprising administration to a subject a suitable amount of a pharmaceutical agent or an antibody which is capable of using an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity, as a target molecule.

In another embodiment the invention is related to a method of preventing adhesion between tendon/ligaments and the surrounding tissue after infection, inflammation and after surgical intervention where adhesion impairs the function of the tissue, comprising administration to a subject a suitable amount of a pharmaceutical agent or an antibody which is capable of using a integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity, as a target molecule.

The invention also relates to a method of stimulating extracellular matrix synthesis and repair by activation or blockage of an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or of the subunit $\alpha 10$ thereof, or of a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity.

In a further aspect the invention relates to a method of in vitro detecting the presence of integrin binding entities, comprising interaction of an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit, with a sample, thereby causing said integrin, subunit $\alpha 10$, or homologue or fragment thereof having similar biological activity, to modulate

the binding to its natural ligand or other integrin binding proteins present in said sample.

The invention also relates to a method of in vitro studying consequences of the interaction of a human
5 heterodimer integrin comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit, with an integrin binding entity and thereby initiate a cellular reaction. Said consequences may be measured as alterations in cellular functions.
10

A still further aspect of the inventions relates to a method of using DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof as a molecular target. In an embodiment of this aspect, a polynucleotide
15 or oligonucleotide hybridises to the DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof, whereby said polynucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$.

20 The invention also relates to a method of using a human heterodimer integrin comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit, or a DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof, as a marker or target molecule during
25 angiogenesis.

BRIEF DESCRIPTION OF THE FIGURES

Fig.1 Affinity purification of the $\alpha 10$ integrin subunit on collagen type II-Sepharose.

30 Fig. 2. Amino acid sequences of peptides from the bovine $\alpha 10$ integrin subunit.

Fig. 3a. Affinitypurification and immunoprecipitation of the integrin subunit $\alpha 10$ from bovine chondrocytes.

35 Fig. 3b. Affinitypurification and immunoprecipitation of the integrin subunit $\alpha 10$ from human chondrocytes.

Fig. 3c. Affinitypurification and immunoprecipitation of the integrin subunit $\alpha 10$ from human chondrosarcoma cells.

5 Fig. 4. A 900 bp PCR-fragment corresponding to the bovine integrin subunit $\alpha 10$

Fig. 5. Schematic map of the three overlapping $\alpha 10$ clones.

Fig. 6. Nucleotide sequence and deduced amino acid sequence of the human $\alpha 10$ integrin subunit.

10 Fig. 7. Northern blot of integrin $\alpha 10$ mRNA.

Fig. 8 Immunoprecipitation of the $\alpha 10$ integrin subunit from human chondrocytes using antibodies against the cytoplasmic domain of $\alpha 10$ (a). Western blot of the $\alpha 10$ associated β -chain (b).

15 Fig. 9. Immunostaining of $\alpha 10$ integrin in human articular cartilage.

Fig. 10 Immunostaining of $\alpha 10$ integrin in 3 day mouse limb cartilage.

20 Fig 11. Immunostaining of $\alpha 10$ integrin in 13.5 day mouse embryo.

Fig 12. Hybridisation of $\alpha 10$ mRNA in various human tissues.

25 Fig. 13 Immunostaining of fascia around tendon (a), skeletal muscle (b) and heart valves (c) in 3 day mouse limb.

Fig. 14. PCR fragments corresponding to $\alpha 10$ integrin subunit from human chondrocytes, human endothelial cells, human fibroblasts and rat tendon.

30 Fig 15. Partial genomic nucleotide sequence of the human integrin subunit $\alpha 10$.

Fig 16. Upregulation of $\alpha 10$ integrin subunit in chondrocytes cultured in alginate.

35 Fig 17. Immunoprecipitation of the $\alpha 10$ integrin subunit from human smooth muscle cells

DETAILED DESCRIPTION OF THE INVENTION

The present invention demonstrate that human and

bovine chondrocytes express a novel, collagen type II-binding integrin in the $\beta 1$ -family. An earlier study presented some evidence for that human chondrosarcoma cells also express this integrin (25). Immunoprecipitation experiments using antibodies against the integrin subunit $\beta 1$ revealed that this novel α -integrin subunit had an apparent molecular weight (M_r) of approximately 160 kDa under reducing conditions, and was slightly larger than the $\alpha 2$ integrin subunit. To isolate this α -subunit collagen type II-binding proteins were affinity purified from bovine chondrocytes. The chondrocyte lysate was first applied to a fibronectin-Sepharose precolumn and the flow through was then applied to a collagen type II-Sepharose column. A protein with M_r of approximately 160 kD was specifically eluted with EDTA from the collagen column but not from the fibronectin column. The M_r of this protein corresponded with the M_r of the unidentified $\beta 1$ -related integrin subunit. The 160 kD protein band was excised from the SDS-PAGE gel, digested with trypsin and the amino acid sequences of the isolated peptides were analysed.

Primers corresponding to isolated peptides amplified a 900 bp PCR-fragment from bovine cDNA which was cloned, sequenced and used for screening of a human articular chondrocyte λ ZapII cDNA library to obtain the human integrin α -subunit homologue. Two overlapping clones, hc1 and hc2 were isolated, subcloned and sequenced. These clones contained 2/3 of the nucleotide sequence including the 3' end of the cDNA. A third clone which contained the 5' end of the $\alpha 10$ cDNA, was obtained using the RACE technique. Sequence analysis of the 160 kD protein sequence showed that it was a member of the integrin α -subunit family and the protein was named $\alpha 10$.

The deduced amino acid sequence of $\alpha 10$ was found to share the general structure of the integrin α -subunits described in previously published reports (6-21). The large extracellular N-terminal part of $\alpha 10$ contains a

seven-fold repeated sequence which was recently predicted to fold into a β -propeller domain (32). The integrin subunit $\alpha 10$ contains three putative divalent cation-binding sites (DxD/NxD/NxxxD) (53), a single spanning transmembrane domain and a short cytoplasmic domain. In contrast to most α -integrin subunits the cytoplasmic domain of $\alpha 10$ does not contain the conserved sequence KxGFF (R/K) R. The predicted amino acid sequence in $\alpha 10$ is KLGFFAH. Several reports indicate that the integrin cytoplasmic domains are crucial in signal transduction (54) and that membrane-proximal regions of both α - and β -integrin cytoplasmic domains are involved in modulating conformation and affinity state of integrins (55-57). It is suggested that the GFFKR motif in α -chains are important for association of integrin subunits and for transport of the integrin to the plasma membrane (58). The KxGFFKR domain has been shown to interact with the intracellular protein calreticulin (59) and interestingly, calreticulin-null embryonic stem cells are deficient in integrin-mediated cell adhesion (60). It is therefore possible that the sequence KLGFFAH in $\alpha 10$ have a key function in regulating the affinity between $\alpha 10\beta 1$ and matrix proteins.

Integrin α subunits are known to share an overall identity of 20-40% (61). Sequence analysis showed that the $\alpha 10$ subunit is most closely related to the I-domain containing α -subunits with the highest identity to $\alpha 1$ (37%) and $\alpha 2$ (35%). The integrins $\alpha 1\beta 1$ and $\alpha 2\beta 1$ are known receptors for both collagens and laminins (24;62;63) and we have also recently demonstrated that $\alpha 2\beta 1$ interacts with the cartilage matrix protein chondroadherin (42). Since $\alpha 10\beta 1$ was isolated on a collagen type II-Sepharose, we know that collagen type II is a ligand for $\alpha 10\beta 1$. We have also shown by affinity purification experiments that $\alpha 10\beta 1$ interacts with collagen type I but it remains to be seen whether laminin or chondroadherin are also ligands for this integrin.

The $\alpha 10$ associated β -chain migrated as the $\beta 1$ integrin subunit both under reducing and non-reducing conditions. To verify that the $\alpha 10$ associated β -chain indeed is $\beta 1$, chondrocyte lysates were immunoprecipitated with
5 antibodies against $\alpha 10$ or $\beta 1$ followed by Western blot using antibodies against the $\beta 1$ -subunit. These results clearly demonstrated that $\alpha 10$ is a member of the $\beta 1$ -integrin family. However, the possibility that $\alpha 10$ combine also with other β -chains can not be excluded..

10 A polyclonal peptide antibody raised against the cytoplasmic domain of $\alpha 10$ precipitated two protein bands with M_r of approximately 160 kD ($\alpha 10$) and 125 kD ($\beta 1$) under reducing conditions. Immunohistochemistry using the $\alpha 10$ -antibody showed staining of the chondrocytes in tis-
15 sue sections of human articular cartilage. The antibody staining was clearly specific since preincubation of the antibody with the $\alpha 10$ -peptide completely abolished the staining. Immunohistochemical staining of mouse limb sections from embryonic tissue demonstrated that $\alpha 10$ is
20 upregulated during condensation of the mesenchyme. This indicate that the integrin subunit $\alpha 10$ is important during the formation of cartilage. In 3 day old mice $\alpha 10$ was found to be the dominating collagen binding integrin subunit which point to that $\alpha 10$ has a key function in
25 maintaining normal cartilage functions.

Expression studies on the protein and mRNA level show that the distribution of $\alpha 10$ is rather restrictive. Immunohistochemistry analyses have shown that $\alpha 10$ integrin subunit is mainly expressed in cartilage but it is
30 also found in perichondrium, periosteum, ossification groove of Ranvier, in fascia surrounding tendon and skeletal muscle and in the tendon-like structures in the heart valves. This distribution point to that $\alpha 10$ integrin subunit is present also on fibroblasts and
35 osteoblasts. PCR amplification of cDNA from different cell types revealed the presence of an alternatively spliced $\alpha 10$ integrin subunit. This spliced $\alpha 10$ was domi-

nating in fibroblasts which suggests that $\alpha 10$ in fibroblasts may have a different function compared to $\alpha 10$ present on chondrocytes.

Expression of the integrin subunit $\alpha 10$ was found to
5 decrease when chondrocytes were cultured in monolayer. In contrast, the expression of $\alpha 10$ was found to increase when the cells were cultured in alginate beads. Since the latter culturing model is known to preserve the phenotype of chondrocytes the results suggest that $\alpha 10$ can function
10 as marker for a differentiated chondrocyte.

Adhesion between tendon/ligaments and the surrounding tissue is a well-known problem after infection, injury and after surgical intervention. Adhesion between tendon and tendon sheets impairs the gliding function and
15 cause considerable problems especially during healing of tendons in e.g. the hand and fingers leading to functional incapacity. The localisation of the $\alpha 10$ integrin subunit in the fascia of tendon and skeletal muscle makes $\alpha 10$ a possible target for drugs and molecules with anti-
20 adhesive properties that could prevent impairment of the function of tendon/ligament. The integrin subunit $\alpha 10$ can also be a target for drugs or molecules with anti-adhesive properties in other tissues where adhesion is a problem.

25

EXAMPLES

Example 1

Affinity purification of the $\alpha 10$ integrin subunit on
30 collagen type II-Sepharose.

Materials and Methods

Bovine chondrocytes, human chondrocytes or human chondrosarcoma cells were isolated as described earlier [Holmvall et al, Exp Cell Res, 221, 496-503 (1995),
35 Camper et al, JBC, 273, 20383-20389 (1998)]. A Triton X-100 lysate of bovine chondrocytes was applied to a fibronectin-Sepharose precolumn followed by a collagen

type II-Sepharose column and the integrin subunit $\alpha 10$ was eluted from the collagen type II-column by EDTA (Camper et al, JBC, 273, 20383-20389 (1998)). The eluted proteins were precipitated by methanol/chloroform, separated by
5 SDS-PAGE under reducing conditions and stained with Coomassie blue. (Camper et al, JBC, 273, 20383-20389 (1998)). Peptides from the $\alpha 10$ protein band were isolated by in-gel digestion with a trypsin and phase liquid chromatography and sequenced by Edman degradation (Camper et
10 al, JBC, 273, 20383-20389 (1998)).

Results

Fig 1 shows EDTA-eluted proteins from the fibronectin-Sepharose (A), flow-through from the collagen type II-Sepharose column (B) and EDTA-eluted proteins from the
15 collagen type II-Sepharose (C). The $\alpha 10$ integrin subunit (160 kDa) which was specifically eluted from the collagen type II column is indicated with an arrow. Figure 2 shows the amino acid sequences of six peptides that were isolated from the bovine integrin subunit $\alpha 10$. Figures 3 a,
20 b, and c show that the $\alpha 10$ integrin subunit is present on bovine chondrocytes (3a), human chondrocytes (3b) and human chondrosarcoma cells (3c). The affinity for collagen type II, the coprecipitation with $\beta 1$ -integrin subunit and the molecular weight of 160 kDa under reducing conditions identify the $\alpha 10$ integrin subunit on the different
25 cells. These results show that $\alpha 10$ can be isolated from chondrocytes and from chondrosarcoma cells.

Example 2

30 Amplification of PCR fragment corresponding to bovine $\alpha 10$ integrin subunit.

Materials and methods

The degenerate primers GAY AAY ACI GCI CAR AC (DNTAQT, forward) and TIA TIS WRT GRT GIG GYT (EPHHSI,
35 reverse) were used in PCR (Camper et al, JBC, 273, 20383-20389 (1998)) to amplify the nucleotide sequence corresponding to the bovine peptide 1 (Figure 2). A 900 bp

PCR-fragment was then amplified from bovine cDNA using an internal specific primer TCA GCC TAC ATT CAG TAT (SAYIQY, forward) corresponding to the cloned nucleotide sequence of peptide 1 together with the degenerate primer ICK RTC CCA RTG ICC IGG (PGHWDR, reverse) corresponding to the bovine peptide 2 (Figure2). Mixed bases were used in positions that were twofold degenerate and inosines were used in positions that are three- or fourfold degenerate. mRNA isolation and cDNA synthesis was done as earlier described (Camper et al, JBC, 273, 20383-20389 (1998)). The purified fragment was cloned, purified and sequenced as earlier described (Camper et al, JBC, 273, 20383-20389 (1998)).

Results

The nucleotide sequence of peptide 1 (Figure 2) was obtained by PCR-amplification, cloning and sequencing of bovine cDNA. From this nucleotide sequence an exact primer was designed and applied in PCR-amplification with degenerate primers corresponding to peptides 2-6 (Figure 2). Primers corresponding to peptides 1 and 2 amplified a 900 bp PCR-fragment from bovine cDNA (Figure 4).

Example 3

Cloning and sequence analysis of the human $\alpha 10$ integrin subunit

Material and methods

The cloned 900bp PCR-fragment, corresponding to bovine $\alpha 10$ -integrin, was digoxigenin-labelled according to the DIG DNA labelling kit (Boehringer Mannheim) and used as a probe for screening of a human articular chondrocyte λ ZapII cDNA library (provided by Michael Bayliss, The Royal Veterinary Basic Sciences, London, UK) (52). Positive clones containing the pBluescript SK+ plasmid with the cDNA insert were rescued from the ZAP vector by *in vivo* excision as described in the ZAP-cDNA[®] synthesis kit (Stratagene). Selected plasmids were purified and

sequenced as described earlier (Camper et al, JBC, 273, 20383-20389 (1998)) using T3, T7 and internal specific primers. To obtain cDNA that encoded the 5' end of $\alpha 10$ we designed the primer AAC TCG TCT TCC AGT GCC ATT CGT GGG (reverse; residue 1254-1280 in $\alpha 10$ cDNA) and used it for rapid amplification of the cDNA 5' end (RACE) as described in the Marathon™ cDNA Amplification kit (Clontech INC., Palo Alto, CA).

Results

Two overlapping clones, hc1 and hc2 (Figure 5), were isolated, subcloned and sequenced. These clones contained 2/3 of the nucleotide sequence including the 3' end of the cDNA. A third clone (racel; Figure 5), which contained the 5' end of the $\alpha 10$ cDNA, was obtained using the RACE technique. From these three overlapping clones of $\alpha 10$ cDNA, 3884 nucleotides were sequenced. The nucleotide sequence and deduced amino acid sequence is shown in Figure 6. The sequence contains a 3504-nucleotide open reading frame that is predicted to encode a 1167 amino acid mature protein. The signal peptide cleavage site is marked with an arrow, human homologues to bovine peptide sequences are underlined and the I-domain is boxed. Metal ion binding sites are indicated with a broken underline, potential N-glycosylation sites are indicated by an asterisk and the putative transmembrane domain is double underlined. The normally conserved cytoplasmic sequence is indicated by a dot and dashed broken underline.

Sequence analysis demonstrate that $\alpha 10$ is a member of the integrin α -subunit family.

Example 4

Identification of a clone containing a splice variant of $\alpha 10$

One clone which was isolated from the human chondrocyte library (see Example 3) contained a sequence that was identical to the sequence of $\alpha 10$ integrin subunit except that the nucleotides between nt positions

2942 and 3055 were deleted. The splice variant of $\alpha 10$ was verified in PCR experiment using primers flanking the splice region (see figure 14).

5 Example 5

Identification of $\alpha 10$ integrin subunit by Northern blot

Material and methods

Bovine chondrocyte mRNA was purified using a QuickPrep® Micro mRNA Purification Kit (Pharmacia Biotech; Uppsala, Sweden), separated on a 1% agarose-formaldehyde gel, transferred to nylon membranes and immobilised by UV-crosslinking. cDNA-probes were ^{32}P -labelled with Random Primed DNA Labeling Kit (Boehringer Mannheim). Filters were prehybridised for 2-4 hours at 42°C in 5x SSE, 5x Denharts solution, 0.1 % SDS, 50 $\mu\text{g/ml}$ salmon sperm DNA and 50% formamide and then hybridised over night at 42°C with the same solution containing the specific probe ($0.5\text{-}1 \times 10^6$ cpm/ml). Specifically bound cDNA-probes were analysed using the phosphorimager system (Fuji). Filters were stripped by washing in 0.1% SDS, for 1 hour at 80°C prior to re-probing. The $\alpha 10$ -integrin cDNA-probe was isolated from the rac1-containing plasmid using the restriction enzymes BamHI (GIBCO BRL) and NcoI (Boehringer Mannheim). The rat $\beta 1$ -integrin cDNA probe was a kind gift from Staffan Johansson, Uppsala, Sweden.

Results

Northern blot analysis of mRNA from bovine chondrocytes showed that a human $\alpha 10$ cDNA-probe hybridised with a single mRNA of approximately 5.4 kb (Figure 7). As a comparison, a cDNA-probe corresponding to the integrin subunit $\alpha 1$ was used. This cDNA-probe hybridised a mRNA-band of approximately 3.5 kb on the same filter. These results show that a cDNA-probe against $\alpha 10$ can be used to identify the $\alpha 10$ integrin subunit on the mRNA level.

Example 6

Preparation of antibodies against the integrin subunit $\alpha 10$

A peptide corresponding to part of the $\alpha 10$ cytoplasmic domain, Ckkipееekreekle (see figure 6) was synthesised and conjugated to keyhole limpet hemocyanin (KLH). Rabbits were immunised with the peptide-KLH conjugate to generate antiserum against the integrin subunit $\alpha 10$. Antibodies recognising $\alpha 10$ were affinity purified on an peptide-coupled column (Innovagen AB).

Example 7

Immunoprecipitation of the integrin subunit $\alpha 10$ from chondrocytes

15 Material and methods

Human chondrocytes were ^{125}I -labelled, lysed with Triton X-100 and immunoprecipitated as earlier described (Holmvali et al, Exp Cell Res, 221, 496-503 (1995), Camper et al, JBC, 273, 20383-20389 (1998)). Triton X-100 lysates of ^{125}I -labeled human chondrocytes were immunoprecipitated with polyclonal antibodies against the integrin subunits $\beta 1$, $\alpha 1$, $\alpha 2$, $\alpha 3$ or $\alpha 10$. The immunoprecipitated proteins were separated by SDS-PAGE (4-12%) under non-reducing conditions and visualised using a phosphor imager. Triton X-100 lysates of human chondrocytes immunoprecipitated with $\alpha 10$ or $\beta 1$ were separated by SDS-PAGE (8%) under non-reducing conditions and analysed by Western blot using the polyclonal $\beta 1$ antibody and chemiluminescent detection as described in Camper et al, JBC, 273, 20383-20389 (1998).

Results

The polyclonal peptide antibody, raised against the cytoplasmic domain of $\alpha 10$, precipitated two protein bands with Mr of approximately 160 kD ($\alpha 10$) and 125 kD ($\beta 1$) under reducing conditions. The $\alpha 10$ associated β -chain migrated as the $\beta 1$ integrin subunit (Figure 8a). To verify that the $\alpha 10$ associated β -chain in chondrocytes

indeed is $\beta 1$, chondrocyte lysates were immunoprecipitated with antibodies against $\alpha 10$ or $\beta 1$ followed by Western blot using antibodies against the $\beta 1$ -subunit (Figure 8b). These results clearly demonstrated that $\alpha 10$ is a member of the $\beta 1$ -integrin family. However, the results do not exclude the possibility that $\alpha 10$ can associate with other β -chains in other situations.

Example 8

Immunohistochemical staining of the integrin subunit $\alpha 10$ in human and mouse cartilage

Material and methods

Frozen sections of adult cartilage (trochlear groove) obtained during surgery (provided by Anders Lindahl, Salgrenska Hospital, Gothenburg, Sweden and frozen sections from of 3 day old mouse limb were fixed and prepared for immunohistochemistry as earlier described (Camper et al, JBC, 273, 20383-20389 (1998)). Expression of $\alpha 10$ integrin subunit was analysed using the polyclonal antibody against the cytoplasmic domain as a primary antibody (see Example 6) and a secondary antibody conjugated to peroxidase.

Results

Figures 9 show immunostaining of human adult articular cartilage.

The $\alpha 10$ -antibody recognising the cytoplasmic domain of $\alpha 10$ stained the chondrocytes in tissue sections of human articular cartilage (A). The staining was depleted when the antibody was preincubated with the $\alpha 10$ - peptide (B). A control antibody recognising the $\alpha 9$ integrin subunit did not bind to the chondrocyte (C).

Figures 10 shows that the $\alpha 10$ antibody stain the majority of chondrocytes in the growing bone anlage (a and b). The $\alpha 10$ antibody also recognised cells in the ossification groove of Ranvier (b), especially the osteoblast in the bone bark which are lining the cartilage in the metaphys are highly positive for $\alpha 10$. The

cells in the ossification groove of Ranvier are believed to be important for the growth in diameter of the bone. The integrin subunit $\alpha 10$ is also highly expressed in perichondrium and periosteum. Cell in these tissues are likely important in the repair of the cartilage tissue. The described localisation of the integrin subunit $\alpha 10$ suggest that this integrin is important for the function of the cartilage tissue.

10 Example 9

Immunohistochemical staining of the integrin subunit $\alpha 10$ during mouse development

Material and methods

Frozen sections from mouse embryos (13.5 days) were investigated for expression of $\alpha 10$ by immunohistochemistry as described in Camper et al, JBC, 273, 20383-20389 (1998). Expression of $\alpha 10$ integrin subunit was analysed using the polyclonal antibody against the cytoplasmic domain as a primary antibody (see Example 6) and a secondary antibody conjugated to peroxidase. The embryo sections were also investigated for expression of integrin subunit $\alpha 1$ (monoclonal antibody from Pharmingen) and collagen type II (monoclonal antibody, kind gift from Dr John Mo, Lund University, Sweden).

25 Results

Figure 11 show that $\alpha 10$ integrin subunit is unregulated in the limb when the mesenchymal cells undergo condensation to form cartilage (a). Especially the edge of the newly formed cartilage has high expression of $\alpha 10$. The formation of cartilage is verified by the high expression of the cartilage specific collagen type II (b). The control antibody against $\alpha 1$ integrin subunit showed only weak expression on the cartilage (c). In other experiments expression of $\alpha 10$ was found in all cartilage containing tissues in the 3 day old mouse including limbs, ribs and vertebrae. The upregulation of $\alpha 10$ during formation of cartilage suggest that this integrin subunit is

important both in the development of cartilage and bone and in the repair of damaged cartilage tissue.

Example 10

5 mRNA expression of $\alpha 10$ in tissues other than articular cartilage

Material and methods

Expression of $\alpha 10$ integrin subunit was examined on the mRNA level in different human tissues. A Northern dot
10 blot with immobilised mRNA from the listed tissues in Figure 12 was hybridised with an $\alpha 10$ integrin cDNA probe isolated from the race 1-containing plasmid using the restriction enzymes *Bam*H1 and *Nco*1. The degree of hybridisation was analysed using a phospho imager. The following
15 symbols denote mRNA level in increasing order: -, +, ++, +++, +++++.

Results

Analysis of the hybridised mRNA showed that $\alpha 10$ was expressed in aorta, trachea, spinal cord, heart,
20 lung, and kidney (Figure 12). All other tissues appeared negative for $\alpha 10$ expression. These results point to a restricted distribution of the $\alpha 10$ integrin subunit.

Example 11

25 Immunohistochemical staining of $\alpha 10$ in fascia around tendon and skeletal muscle and in tendon structures in heart valves.

Materials and methods

Frozen sections of adult cartilage (trochlear
30 groove) obtained during surgery (provided by Anders Lindahl, Salgreńska Hospital, Gothenburg, Sweden and frozen sections from of 3 day old mouse limb were fixed and prepared for immunohistochemistry as earlier described (Camper et al, JBC, 273, 20383-20389 (1998)). Expression
35 of $\alpha 10$ integrin subunit was analysed using the polyclonal antibody against the cytoplasmic domain as a pri-

mary antibody (see Example 6) and a secondary antibody conjugated to peroxidase.

Results

As shown in figures 13 expression of $\alpha 10$ was found in the fascia surrounding tendon (a) and skeletal muscle (b) and in the tendon structures in the heart valves (c). This localisation suggest that $\alpha 10$ can bind to other matrix molecules in addition to the cartilage specific collagen type II. The localisation of the integrin $\alpha 10$ on the surface of tendons indicate that $\alpha 10$ can be involved in unwanted adhesion that often occurs between tendon/ligaments and the surrounding tissue after infection, injury or after surgery.

Example 12

mRNA expression of $\alpha 10$ integrin subunit in chondrocytes, endothelial cells and fibroblasts.

Material and methods

Isolation of mRNA, synthesis of cDNA and PCR amplification was done as earlier described (Camper et al, JBC, 273, 20383-20389 (1998)).

Results

Figure 14 shows PCR amplification of $\alpha 10$ cDNA from human articular chondrocytes (lanes A6 and B1), human umbilical vein endothelial cells (lane A2), human fibroblasts (lane A4) and rat tendon (Fig 14b, lane B2). Lanes 1, 3, and 5 in figure 14 A show amplified fragments corresponding to the integrin subunit $\alpha 2$ in endothelial cells, fibroblasts and chondrocytes, respectively. cDNA-primers corresponding to the $\alpha 10$ sequence positions nt 2919-2943 (forward) and nt 3554-3578 (reverse) (see Figure 6) were used to amplify $\alpha 10$ cDNA from the different cells. The figure shows that $\alpha 10$ was amplified in all three cell types. Two fragments of $\alpha 10$ was amplified which represent the intact form of $\alpha 10$ (larger fragment) and a splice variant (smaller fragment). The larger frag-

ment was dominating in chondrocytes while the smaller fragment was more pronounced in tendon (B2).

Example 13

5 Construction of $\alpha 10$ mammalian expression vector.

The full length protein coding sequence of $\alpha 10$ (combined from 3 clones, see figure 6) was inserted into the mammalian expression vector, pcDNA3.1/Zeo (Invitrogen). The vector contains SV40 promoter and Zeosin selection
10 sequence. The $\alpha 10$ containing expression vector was transfected into cells that express the $\beta 1$ -integrin subunit but lack expression of the $\alpha 10$ subunit. Expression of the $\alpha 10$ integrin subunit on the cell surface can be analysed by immunoprecipitation and/or flow cytometry using anti-
15 bodies specific for $\alpha 10$. The ligand binding capacity and the function of the inserted $\alpha 10$ integrin subunit can be demonstrated in cell adhesion experiment and in signalling experiments.

20 Example 14

Construction of mammalian expression vector containing a splice variant of $\alpha 10$.

The full length protein coding sequence of the splice variant of $\alpha 10$ (nt 2942-nt3055 deleted) was
25 inserted into the mammalian expression vector pcDNA3 (see Example 13). Expression and function of the splice variant can be analysed as described in example 13 and compared with the intact $\alpha 10$ integrin subunit.

30 Example 15

Partial isolation and characterisation of the $\alpha 10$ integrin genomic DNA

Material and methods

Human $\alpha 10$ cDNA, isolated from the racel-containing
35 plasmid using the restriction enzymes *Bam*HI (GIBCO BRL) and *Nco*I (Boehringer Mannheim), was 32 P-labelled and used as a probe for screening of a mouse 129 cosmid library

(provided by Reinhard Fässler, Lund University). Positive clones were isolated and subcloned. Selected plasmids were purified and sequenced as described earlier (Camper et al, JBC, 273, 20383-20389 (1998)) using T3, T7 and
5 internal specific primers. Primers corresponding to mouse genomic DNA were then constructed and used in PCR to amplify and identify the genomic sequence of $\alpha 10$ from the cosmid clones.

Results

10 Figure 15 shows 7958 nt of the $\alpha 10$ gene. This partial genomic DNA sequence of $\alpha 10$ integrin contains 8 exons, and a Kozak sequence. The mouse genomic $\alpha 10$ sequence was used to generate a targeting vector for knockout experiments.

15

Example 16

Upregulation of $\alpha 10$ integrin subunit in chondrocytes cultured in alginate beads

Material and methods

20 Human chondrocytes cultured in monolayer for 2 weeks were detached with trypsin-EDTA and introduced into alginate beads. Chondrocytes cultured in alginate are known to preserve their phenotype while chondrocytes cultured in monolayer are dedifferentiated. After 11 days chondrocytes cultured either in alginate or on monolayer were
25 isolated and surface labelled with ^{125}I . The $\alpha 10$ integrin subunit was then immunoprecipitated with polyclonal antibodies recognising the cytoplasmic domain of $\alpha 10$ (see Example 6 and Camper et al, JBC, 273, 20383-20389
30 (1998)).

Results

As shown in figure 16 chondrocytes cultured in alginate beads (lanes 3 and 4) upregulated their protein expression of $\alpha 10\beta 1$. This was in contrast to chondrocytes
35 cultured in monolayer (lanes 1 and 2) which had a very low expression of $\alpha 10\beta 1$. Immunoprecipitation with ab control antibody is shown in lanes 1 and 3. It is known that

chondrocytes preserve their cartilage specific matrix production in alginate cultures but not in monolayer culture which point to that alginate preserve the phenotype of chondrocytes. These results support that $\alpha 10$ integrin subunit can be used as a marker for differentiated chondrocytes.

Example 17

Immunoprecipitation of the $\alpha 10$ integrin subunit from human smooth muscle cells.

Material and methods

Human smooth muscle cells were isolated from human aorta. After one week in culture the cells were ^{125}I -labelled, lysed and immunoprecipitated with antibodies against the integrin subunit $\beta 1$ (lane 1), $\alpha 1$ (lane 2), $\alpha 2$ (lane 3), $\alpha 10$ (lane 4), $\alpha 3$ (lane 5), control (lane 6) (Figure 17). The experiment was done as described in Example 7.

Results

The $\alpha 10$ antibody precipitated two bands from the smooth muscle cells corresponding to the $\alpha 10$ and the $\beta 1$ integrin subunit (Fig. 17).

Example 18

Construction of bacterial expression vector containing sequence for $\alpha 10$ splice region:

A plasmid for intracellular expression in *E. coli* of the alternatively spliced region (amino acid pos. 952-986, SEQ. ID 1) was constructed as described. The alternatively spliced region were back-translated using the *E. coli* high frequency codon table, creating a cDNA sequence of 96% identity with the original sequence (SEQ. ID 1 nucleotide pos 2940-3044). Using sequence overlap extension (Horton et al., Biotechniques 8:528, 1990) primer $\alpha 10\text{pfor}$ (tab. I) and $\alpha 10\text{prev}$ (tab. I) was used to generate a double stranded fragment encoding the $\alpha 10$ amino acid sequence. This fragment was used as a PCR

template with primers $\alpha 10$ pfor2 (tab. I) and $\alpha 10$ prev2 (tab. I) in order to generate restriction enzyme site for sub-cloning in a pET vector containing the Z-domain of staphylococcal protein A, creating a fusion of the $\alpha 10$ spliced region with the amino terminal of the Z-domain with trombin cleavage site residing in-between. The fragment generated in the second PCR reaction is shown (SEQ ID No. 3) also indicating the unique restriction enzymes used for sub-cloning in the expression vector.

10

Table I

$\alpha 10$ pfor	5'- GTTTCAGAACCTGGGTTGCTACGTTGTTCCGGTCTGATCATCTCCGC TCTGCTGCCGGCTGT-3'
$\alpha 10$ pfor2	5'-GGGGCATATGGTTCAGAACCTGGGTTGCTACGTTG-3'
$\alpha 10$ prev	5'- GATAACCTGGGACAAGCTTAGGAAGTAGTTACCACCGTGAGCAACAG CCGGCAGCAGAGCGGA-3'
$\alpha 10$ prev2	5'- GGGGGGATCCGCGCGGCACCAGGCCGCTGATAACCTGGGACAAGCTT AGGAAGT-3'

REFERENCES

1. Springer, T.A. (1990) *Nature* **346**, 425-434
2. Ruoslahti, E. (1991) *J.Clin.Invest.* **87**, 1-5
3. Hynes, R.O. (1992) *Cell* **69**, 11-25
- 5 4. Hemler, M.E. (1988) *Immunol.Today* **9**, 109-113
5. Yamada, K.M. (1991) *J.Biol.Chem.* **266**, 12809-12812
6. Palmer, E.L., Ruegg, C., Ferrando, R., Pytela, R.,
and Sheppard, D. (1993) *J.Cell Biol.* **123**, 1289-1297
7. Takada, Y., Elices, M.J., Crouse, C., and Hemler,
10 M.E. (1989) *EMBO J.* **8**, 1361-1368
8. Poncz, M., Eisman, R., Heidenreich, R., Silver, S.M.,
Vilaire, G., Surrey, S., Schwartz, E., and Bennett,
J.S. (1987) *J.Biol.Chem.* **262**, 8476-8482
9. Larson, R.S., Corbi, A.L., Berman, L., and Springer,
15 T. (1989) *J.Cell Biol.* **108**, 703-712
10. Corbi, A.L., Kishimoto, T.K., Miller, L.J., and
Springer, T.A. (1988) *J.Biol.Chem.* **263**, 12403-12411
11. Argaves, W.S., Suzuki, S., Arai, H., Thompson, K.,
Pierschbacher, M.D., and Ruoslahti, E. (1987) *J.Cell*
20 *Biol.* **105**, 1183-1190...
12. Corbi, A.L., Miller, L.J., O'Connor, K., Larson,
R.S., and Springer, T.A. (1987) *EMBO J.* **6**, 4023-4028
13. Briesewitz, R., Epstein, M.R., and Marcantonio, E.E.
(1993) *J.Biol.Chem.* **268**, 2989-2996
- 25 14. Ziober, B.L., Vu, M.P., Waleh, N., Crawford, J., Lin,
C.S., and Kramer, R.H. (1993) *J.Biol.Chem.* **268**,
26773-26783
15. Hogervorst, F., Kuikman, I., van Kessel, A.G., and
Sonnenberg, A. (1991) *Eur.J.Biochem.* **199**, 425-433
- 30 16. Takada, Y. and Hemler, M.E. (1989) *J.Cell Biol.* **109**,
397-407
17. Takada, Y., Murphy, E., Pil, P., Chen, C., Ginsberg,
M.H., and Hemler, M.E. (1991) *J.Cell Biol.* **115**,
257-266
- 35 18. Van der Vieren, M., Le Trong, H., Wood, C.L., Moore,
P.F., St.John, T., Staunton, D.E., and Gallatin, W.M.
(1995) *Immunity.* **3**, 683-690

19. Schnapp, L.M., Breuss, J.M., Ramos, D.M., Sheppard, D., and Pytela, R. (1995) *J.Cell Sci.* 108, 537-544
20. Shaw, S.K., Cepek, K.L., Murphy, E.A., Russell, G.J., Brenner, M.B., and Parker, C.M. (1994) *J.Biol.Chem.* 269, 6016-6025
- 5 21. Suzuki, S., Argraves, W.S., Arai, H., Languino, L.R., Pierschbacher, M.D., and Ruoslahti, E. (1987) *J.Biol.Chem.* 262, 14080-14085
22. Ignatius, M.J., Large, T.H., Houde, M., Tawil, J.W., Barton, A., Esch, F., Carbonetto, S., and Reichardt, L.F. (1990) *J.Cell Biol.* 111, 709-720
- 10 23. Gullberg, D., Gehlsen, K.R., Turner, D.C., Åhlén, K., Zijenah, L.S., Barnes, M.J., and Rubin, K. (1992) *EMBO J.* 11, 3865-3873
- 15 24. Staaz, W.D., Rajpara, S.M., Wayner, E.A., Carter, W.G., and Santoro, S.A. (1989) *J.Cell Biol.* 108, 1917-1924
25. Holmvall, K., Camper, L., Johansson, S., Rubin, K., Kimura, J.H., and Lundgren-Åkerlund, E. (1995) *Exp.Cell Res.* 221, 496-503
- 20 26. Forsberg, E., Ek, B., Engström, Å., and Johansson, S. (1994) *Exp.Cell Res.* 213, 183-190
27. Wayner, E.A. and Carter, W.G. (1987) *J.Cell Biol.* 105, 1873-1884
- 25 28. Weitzman, J.B., Pasqualini, R., Takada, Y., and Hemler, M.E. (1993) *J.Biol.Chem.* 268, 8651-8657
29. Elices, M.J. and Hemler, M.E. (1989) *Proc.Natl.Acad.Sci.U.S.A.* 86, 9906-9910
- 30 30. Languino, L.R., Colella, S., Zanetti, A., Andrieux, A., Ryckewaert, J.J., Charon, M.H., Marchisio, P.C., Plow, E.F., Ginsberg, M.H., Marguerie, G., and et al (1989) *Blood* 73, 734-742
31. Tuckwell, D.S., Humphries, M.J., and Brass, A. (1994) *Cell Adhes.Comm.* 2, 385-402
- 35 32. Springer, T.A. (1997) *Proc.Natl.Acad.Sci.U.S.A.* 94, 65-72

33. Colombatti, A., Bonaldo, P., and Doliana, R. (1993) Matrix 13, 297-306
34. Lee, C.H., Bradley, G., and Ling, V. (1995) Cell Growth Differ. 6, 347-354
- 5 35. Calderwood, D.A., Tuckwell, D.S., and Humphries, M.J. (1995) Biochem.Soc.Trans. 23, 504S
36. Kern, A., Eble, J., Golbik, R., and Kuhn, K. (1993) Eur.J.Biochem. 215, 151-159
37. Tuckwell, D.S., Reid, K.B., Barnes, M.J., and
10 Humphries, M.J. (1996) Eur.J.Biochem. 241, 732-739
38. Kamata, T. and Takada, Y. (1994) J.Biol.Chem. 269, 26006-26010
39. Dürr, J., Goodman, S., Potocnik, A., von der Mark, H., and von der Mark, K. (1993) Exp.Cell Res. 207,
15 235-244
40. Salter, D.M., Hughes, D.E., Simpson, R., and Gardner, D.L. (1992) Br.J.Rheumatol. 31, 231-234
41. Woods, V.L.J., Schreck, P.J., Gesink, D.S., Pacheco, H.O., Amiel, D., Akeson, W.H., and Lotz, M. (1994) Arthritis Rheum. 37, 537-544
20
42. Camper, L., Heinegård, D., and Lundgren-Åkerlund, E. (1997) J.Cell Biol 138, 1159-1167
43. Hemler, M.E., Sanchez Madrid, F., Flotte, T.J., Krensky, A.M., Burakoff, S.J., Bhan, A.K., Springer, T.A., and Strominger, J.L. (1984) J.Immunol. 132, 3011-3018
25
44. Bottger, B.A., Hedin, U., Johansson, S., and Thyberg, J. (1989) Differentiation. 41, 158-167
45. Sommarin, Y. and Heinegård, D. (1983) Biochem.J. 214, 777-784
30
46. Häuselmann, H.J., Aydelotte, M.B., Schumacher, B.L., Kuettner, K.E., Gitelis, S.H., and Thonar, E.J.M.A. (1992) Matrix 12, 116-129
47. Miller, E.J. (1972) Biochemistry 11, 4903-4909
- 35 48. Wessel, D. and Flugge, U.I. (1984) Anal.Biochem. 138, 141-143

49. Blobel, G. and Dobberstein, B. (1975) *J.Cell Biol.* 67, 835-851
50. Hellman, U. (1997) in *Protein structure analysis. Preparation, characterization, and microsequencing* (Kamp, R.M., Choli-Papadopoulou, T., and Wittmann-Liebold, B., eds) pp. 97-104, Springer-Verlag, Heidelberg
51. Charles, I.G., Palmer, R.M., Hickery, M.S., Bayliss, M.T., Chubb, A.P., Hall, V.S., Moss, D.W., and Moncada, S. (1993) *Proc.Natl.Acad.Sci.U.S.A.* 90, 11419-11423
52. Tuckwell, D.S., Brass, A., and Humphries, M.J. (1992) *Biochem.J.* 285, 325-331
53. Dedhar, S. and Hannigan, G.E. (1996) *Curr.Opin.Cell Biol.* 8, 657-669
54. Hughes, P.E., O'Toole, T.E., Ylanne, J., Shattil, S.J., and Ginsberg, M.H. (1995) *J.Biol.Chem.* 270, 12411-12417
55. Puzon McLaughlin, W., Yednock, T.A., and Takada, Y. (1996) *J.Biol.Chem.* 271, 16580-16585
56. O'Toole, T.E., Katagiri, Y., Faull, R.J., Peter, K., Tamura, R., Quaranta, V., Loftus, J.C., Shattil, S.J., and Ginsberg, M.H. (1994) *J.Cell Biol.* 124, 1047-1059
57. De Melker, A.A., Kramer, D., Kuikman, I., and Sonnenberg, A. (1997) *Biochem J* 529-537
58. Rojiani, M.V., Finlay, B.B., Gray, V., and Dedhar, S. (1991) *Biochemistry* 30, 9859-9866
59. Coppolino, M.G., Woodside, M.J., Demarex, N., Grinstein, S., St Arnaud, R., and Dedhar, S. (1997) *Nature* 386, 843-847
60. Hynes, R.O. (1992) *Curr.Opin.Genet.Dev.* 2, 621-624
61. Santoro, S.A. (1986) *Cell* 46, 913-920
62. Languino, L.R., Gehlsen, K.R., Wayner, E., Carter, W.G., Engvall, E., and Ruoslahti, E. (1989) *J.Cell Biol.* 109, 2455-2462

63. Yokosaki, Y., Monis, H., Chen, J., and Sheppard, D.
(1996) J.Biol.Chem. 271, 24144-24150

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3884 base pairs
(B) TYPE: nucleic acid and amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (E) ORGANISM: human
(F) CELLTYPE: chondrocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 1:

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3001 -----+-----+-----+-----+-----+ 3060
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43

(2) INFORMATION FOR SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3779 base pairs
- (B) TYPE: nucleic acid and amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (E)

(i) MOLECULAR TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (B) CELLTYPE: chondrocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO. 2:

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44

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481 -----+-----+-----+-----+-----+ 540
TCGGACCGTGGGTGACGGGTGCGACGGGTGTATGTACCTACAACAGTAACAGAACCTA

a S L A P T A Q R C P T Y M D V V I V L D -
GGCTCCAACAGCATCTACCCCTGGTCTGAAGTTCAGACCTTCCTACGAAGACTGGTAGGG
541 -----+-----+-----+-----+-----+ 600
CCGAGGTTGTCGTAGATGGGACCAGACTTCAAGTCTGGAAGGATGCTTCTGACCATCCC

a G S N S I Y P W S E V Q T F L R R L V G -
AAACTGTTTATTGACCCGAAACAGATACAGGTGGGACTGGTACAGTATGGGGAGAGCCCT
601 -----+-----+-----+-----+-----+ 660
TTTGACAAATAACTGGGTCTTGTCTATGTCCACCCTGACCATGTCATACCCCTCTCGGGA

a K L F I D P E Q I Q V G L V Q Y G E S F -
GTACATGAGTGGTCCCTGGGAGATTTCCGAACGAAGGAAGTGGTGAGAGCAGCAAAG
661 -----+-----+-----+-----+-----+ 720
CATGTACTCACCAGGACCCCTCTAAAGGCTTGCTTCTTCTTCACTCTCGTCGTTTC

a V H E W S L G D F R T K E E V V R A A K -
AACCTCAGTCGGCGGGAGGACGAGAAACAAAGACTGCCCAAGCAATAATGGTGGCCTGC
721 -----+-----+-----+-----+-----+ 780
TTGGAGTCAGCCGCCCTCCCTGCTCTTTGTTTCTGACGGGTTCGTATTACCACCGGACG

a N L S R R E G R E T K T A Q A I M V A C -
ACAGAAGGGTTCAGTCAGTCCCATGGGGGCGACCCGAGGCTGCCAGGCTACTGGTGGTT
781 -----+-----+-----+-----+-----+ 840
TGTCTTCCCAAGTCAGTCAGGATACCCCGGCTGGGCTCCGACGGTCCGATGACCACCAA

a T E G F S Q S H G G R P E A A R L L V V -
GTCACTGATGGAGAGTCCCATGATGGAGAGGAGCTTCTGCAGCACTAAAGGCCTGTGAG
841 -----+-----+-----+-----+-----+ 900
CAGTGACTACCTCTCAGGGTACTACCTCTCCTCGAAGGACGTCGTGATTTCCGGACACTC

a V T D G E S H D G E E L P A A L K A C E -
GCTGGAAGAGTGACAGCTATGGGATTGCAGTCTTGGTCACTACCTCCGGCGGCAGCGA
901 -----+-----+-----+-----+-----+ 960
CGACCTTCTCACTGTGCGATACCCTAACGTCAGGAACCACTGATGGAGGCCGCGCTCGCT

a A G R V T R Y G I A V L G H Y L R R Q R -
GATCCCAGCTCTTTCCTGAGAGAAATTAGAACTATTGCCAGTGATCCAGATGAGCGATT
961 -----+-----+-----+-----+-----+ 1020
CTAGGGTCGAGAAAGGACTCTCTTAATCTTGATAACGGTCACTAGGTCTACTCGCTAAG

a D P S S F L R E I R T I A S D P D E R F -
TTCTTCAATGTCACAGATGAGGCTGCTCTGACTGACATTGTGGATGCACTAGGAGATCGG
1021 -----+-----+-----+-----+-----+ 1080
AAGAAGTTACAGTGTCTACTCCGACGAGACTGACTGTAACACCTACGTGATCCTCTAGCC

a F F N V T D E A A L T D I V D A L G D R -
ATTTTGGCCTTGAAGGGTCCCATGCAGAAAACGAAAGCTCCTTTGGGCTGGAATGTCT
1081 -----+-----+-----+-----+-----+ 1140
TAAAAACCGAACTTCCCAGGGTACGTCTTTTGCTTTCGAGGAAACCCGACCTTTACAGA

45

a I F G L E G S H A E N E S S F G L E M S -
CAGATTGGTTTCTCCACTCATCGGCTAAAGGATGGGATTCTTTTGGGATGGTGGGGGCC
1141 -----+-----+-----+-----+-----+ 1200
GTCTAACCAAAGAGGTGAGTAGCCGATTTCCTACCCTAAGAAAAACCTACCACCCCGG

a Q I G F S T H R L K D G I L F G M V G A -
TATGACTGGGGAGGCTCTGTGCTATGGCTTGAAGGAGGCCACCGCCTTTTCCCCCACGA
1201 -----+-----+-----+-----+-----+ 1260
ATACTGACCCCTCCGAGACACGATACCGAACTTCTCCGGTGGCGAAAGGGGGTGCT

a Y D W G G S V L W L E G G H R L F P P R -
ATGGCACTGGAAGACGAGTTCCCCCTGCACTGCAGAACCATGCAGCCTACCTGGGTAC
1261 -----+-----+-----+-----+-----+ 1320
TACCGTGACCTTCTGCTCAAGGGGGACGTGACGTCTTGCTACGTGGATGGACCCAATG

a M A L E D E F P P A L Q N H A A Y L G Y -
TCTGTTTCTTCCATGCTTTTGGGGGTGGACGCCGCTGTTTCTCTCTGGGGCTCCTCGA
1321 -----+-----+-----+-----+-----+ 1380
AGACAAAGAAGGTACGAAAACGCCCCACCTGCGGCGACAAAGAGAGACCCCGAGGAGCT

a S V S S M L L R G G R R L F L S G A P R -
TTTAGACATCGAGGAAAAGTCATCGCCTTCCAGCTTAAGAAAGATGGGGCTGTGAGGGTT
1381 -----+-----+-----+-----+-----+ 1440
AAATCTGTAGCTCCTTTTCAGTAGCGGAAGGTGGAATTCTTCTACCCCGACACTCCCAA

a F R H R G K V I A F Q L K K D G A V R V -
GCCCAGAGCCTCCAGGGGAGCAGATTGGTTCATACTTTGGCAGTGAGCTCTGCCCATTG
1441 -----+-----+-----+-----+-----+ 1500
CGGGTCTCGGAGTCCCCCTCGTCTAACCAAGTATGAAACCGTCACTCGAGACGGGTAAAC

a A Q S L Q G E Q I G S Y F G S E L C P L -
GATACAGATAGGGATGGAACAACTGATGTCTTACTTGTGGCTGCCCCCATGTTCTGGGA
1501 -----+-----+-----+-----+-----+ 1560
CTATGTCTATCCCTACCTTGTGACTACAGAATGAACACCGACGGGGGTACAAGGACCCT

a D T D R D G T T D V L L V A A P M F L G -
CCCCAGAACAAGGAAACAGGACGTGTTTATGTGTATCTGGTAGGCCAGCAGTCCTTGCTG
1561 -----+-----+-----+-----+-----+ 1620
GGGGTCTTGTTCTTTGTCTGCACAAATACACATAGACCATCCGGTCTGCAGGAACGAC

a P Q N K E T G R V Y V Y L V G Q Q S L L -
ACCCTCCAAGGAACACTTCAGCCAGAACCCCCAGGATGCTCGGTTTGGCTTTGCCATG
1621 -----+-----+-----+-----+-----+ 1680
TGGGAGGTTCTTGTGAAGTCGGTCTTGGGGGGTCTACGAGCCAAACCGAAACGGTAC

a T L Q G T L Q P E P P Q D A R F G F A M -
GGAGCTCTCCTGATCTGAACCAAGATGGTTTGTGCTGATGTGGCTGTGGGGCGCCTCTG
1681 -----+-----+-----+-----+-----+ 1740
CCTCGAGAAGGACTAGACTTGGTTCTACCAAAACGACTACACCGACACCCCGCGGAGAC

a G A L P D L N Q D G F A D V A V G A P L -
GAAGATGGGCACCAGGGAGCACTGTACCTGTACCATGGAACCCAGAGTGGAGTCAGGCCC
1741 -----+-----+-----+-----+-----+ 1800
CTTCTACCCGTGGTCCCTCGTGACATGGACATGGTACCTTGGGTCTCACCTCAGTCCGGG

46

a E D G H Q G A L Y L Y H G T Q S G V R P -
CATCCTGCCCAGAGGATTGCTGCTGCCTCCATGCCACATGCCCTCAGCTACTTTGGCCGA
1801 -----+-----+-----+-----+-----+ 1860
GTAGGACGGGTCTCCTAACGACGACGGAGGTACGGTGTACGGGAGTCGATGAAACCGGT

a H P A Q - R I A A A S M P H A L S Y F G R -
AGTGTGGATGGTGGCTAGATCTGGATGGAGATGATCTGGTGGATGTGGCTGTGGGTGCC
1861 -----+-----+-----+-----+-----+ 1920
TCACACCTACCAGCCGATCTAGACCTACCTCTACTAGACCAGCTACACCGACACCCACGG

a S V D G R L D L D G D D L V D V A V G A -
CAGGGGGCAGCCATCTGCTCAGCTCCCGGCCCATTTGTCCATCTGACCCCATCACTGGAG
1921 -----+-----+-----+-----+-----+ 1980
GTCCCCCTCGGTAGGACGAGTCGAGGGCCGGTAACAGGTAGACTGGGGTAGTGACCTC

a Q G A A I L L S S R P I V H L T P S L E -
GTGACCCACAGGCCATCAGTGTGGTTCAGAGGGACTGTAGGCGGCGAGGCCAAGAAGCA
1981 -----+-----+-----+-----+-----+ 2040
CACTGGGGTGTCCGGTAGTCACACCAAGTCTCCCTGACATCCGCGCTCCGGTTCTTCGT

a V T P Q A I S V V Q R D C R R R G Q E A -
GTCTGTCTGACTGCAGCCCTTTGCTTCCAAGTGACCTCCCGTACTCCTGGTCGCTGGGAT
2041 -----+-----+-----+-----+-----+ 2100
CAGACAGACTGACGTCGGGAAACGAAGGTTCAGTGGAGGGCATGAGGACCAGCGACCCCTA

a V C L T A A L C F Q V T S R T P G R W D -
CACCAATTCTACATGAGGTTACCGCATCACTGGATGAATGGACTGCTGGGGCACGTGCA
2101 -----+-----+-----+-----+-----+ 2160
GTGGTTAAGATGTACTCCAAGTGGCGTAGTGACCTACTTACCTGACGACCCCGTGACGT

a H Q F Y M R F T A S L D E W T A G A R A -
GCATTTGATGGCTCTGGCCAGAGTTGTCCCTCGGAGGCTCCGGCTCAGTGTGGGGAAT
2161 -----+-----+-----+-----+-----+ 2220
CGTAAACTACCGAGACCGGTCTCCAACAGGGGAGCCTCCGAGGCCGAGTCACACCCCTTA

a A F D G S G Q R L S P R R L R L S V G N -
GTCACCTGTGAGCAGCTACACTTCCATGTGCTGGATACATCAGATTACCTCCGGCCAGTG
2221 -----+-----+-----+-----+-----+ 2280
CAGTGAACACTCGTCGATGTGAAGGTACACGACCTATGTAGTCTAATGGAGGCCGGTCAC

a V T C E Q L H F H V L D T S D Y L R P V -
GCCTTGACTGTGACCTTTGCCTTGGACAATACTACAAAGCCAGGGCCTGTGCTGAATGAG
2281 -----+-----+-----+-----+-----+ 2340
CGGAACTGACACTGGAAACGGAACCTGTTATGATGTTTCGGTCCCGGACACGACTTACTC

a A L T V T F A L D N T T K P G P V L N E -
GGCTCACCCACCTCTATACAAAAGCTGGTCCCCTTCTCAAAGGATTGTGGCCCTGACAAT
2341 -----+-----+-----+-----+-----+ 2400
CCGAGTGGGTGGAGATATGTTTTCGACCAGGGGAAGAGTTTCTAACACCGGGACTGTTA

a G S P T S I Q K L V P F S K D C G P D N -
GAATGTGTCACAGACCTGGTGCTTCAACTGAATATGGACATCAGAGGCTCCAGGAAGGCC
2401 -----+-----+-----+-----+-----+ 2460
CTTACACAGTGTCTGGACCACGAAGTTCACCTTATACCTGTAGTCTCCGAGGTCCTTCCGG

47

a E C V T D L V L Q V N M D I R G S R K A -
CCATTTGTGGTTCGAGGTGGCCGGCGGAAAGTGCTGGTATCTACAACCTCTGGAGAACAGA
2461 -----+-----+-----+-----+-----+-----+ 2520
GGTAAACACCAAGCTCCACCGGCCCTTTACGACCATAGATGTTGAGACCTCTTGTCT

a P F V V R G G R R K V L V S T T L E N R -
AAGGAAAATGCTTACAATACGAGCCTGAGTATCATCTTCTCTAGAAACCTCCACCTGGCC
2521 -----+-----+-----+-----+-----+-----+ 2580
TTCCTTTTACGAATGTTATGCTCGGACTCATAGTAGAAGAGATCTTTGGAGGTGGACCGG

a K E N A Y N T S L S I I F S R N L H L A -
AGTCTCACTCCTCAGAGAGAGAGCCCAATAAAGGTGGAATGTGCCGCCCTTCTGCTCAT
2581 -----+-----+-----+-----+-----+-----+ 2640
TCAGAGTGAGGAGTCTCTCTCTCGGGTTATTTCCACCTTACACGGCGGGGAAGACGAGTA

a S L T P Q R E S P I K V E C A A P S A H -
GCCCCGCTCTGCAGTGTGGGGCATCCTGTCTTCCAGACTGGAGCCAAGGTGACCTTTCTG
2641 -----+-----+-----+-----+-----+-----+ 2700
CGGGCCGAGACGTCACACCCGTTAGGACAGAAGGTCTGACCTCGGTTCCACTGGAAAGAC

a A R L C S V G H P V F Q T G A K V T F L -
CTAGAGTTTGAGTTTAGCTGCTCCTCTCTCCTGAGCCAGGTCTTTGGGAAGCTGACTGCC
2701 -----+-----+-----+-----+-----+-----+ 2760
GATCTCAAACCTCAAATCGACGAGGAGAGAGGACTCGGTCCAGAAACCTTCGACTGACGG

a L E F E F S C S S L L S Q V F G K L T A -
AGCAGTGACAGCCTGGAGAGAAATGGCACCCTTCAAGAAAACACAGCCAGACCTCAGCC
2761 -----+-----+-----+-----+-----+-----+ 2820
TCGTCAGTGTCTGGACCTCTCTTTACCGTGGGAAGTTCTTTTGTGTCGGGTCTGGAGTCGG

a S S D S L E R N G T L Q E N T A Q T S A -
TACATCCAATATGAGCCCCACCTCCTGTTCTCTAGTGAGTCTACCTGCACCGCTATGAG
2821 -----+-----+-----+-----+-----+-----+ 2880
ATGTAGGTTTACTCGGGGTGGAGGACAAGAGATCACTCAGATGGGACGTGGCGTACTC

a Y I Q Y E P H L L F S S E S T L H R Y E -
GTTCACCCATATGGGACCCTCCAGTGGGTCTGGCCCAGAATTCAAACCACTCTCAGG
2881 -----+-----+-----+-----+-----+-----+ 2940
CAAGTGGGTATACCCTGGGAGGGTCACCCAGGACCGGTCTTAAGTTTGGTGAGAGTCC

a V H P Y G T L P V G P G P E F K T T L R -
ACTAACAATGCAAGCTGCATAGTGAGAACCTGACTGAACCCCGAGGCCACCTGTGCAT
2941 -----+-----+-----+-----+-----+-----+ 3000
TGATTGTTACGTTTCGACGTATCACGTCTTGGACTGACTTGGGGGTCCGGGTGGACACGTA

a T N N A S C I V Q N L T E P P G P P V H -
CCAGAGGAGCTTCAACACACAACAGACTGAATGGGAGCAATACTCAGTGTGAGGTGGTG
3001 -----+-----+-----+-----+-----+-----+ 3060
GGTCTCCTCGAAGTTGTGTGTTGTCTGACTTACCTCGTTATGAGTCACAGTCCACCAC

a P E E L Q H T N R L N G S N T Q C Q V V -
AGGTGCCACCTTGGGAGCTGGCAAAGGGGACTGAGGTCTCTGTGGACTATTGAGGCTG
3061 -----+-----+-----+-----+-----+-----+ 3120
TCCACGGTGGAACCCGTCGACCGTTTCCCTGACTCCAGAGACAACCTGATAACTCCGAC

48

a R C H L G Q L A K G T E V S V G L L R L -
GTTCAATGAATTTTCCGAAGAGCCAAGTTCAAGTCCCTGACGGTGGTCAGCACCTTT
3121 -----+-----+-----+-----+-----+ 3180
CAAGTGTTACTTAAAAAGGCTTCTCGGTTCAAGTTCAAGGACTGCCACCAGTCGTGGAAA

a V H N E F F R R A K F K S L T V V S T F -
GAGCTGGGAACCGAAGAGGGCAGTGTCTACAGCTGACTGAAGCCTCCCGTTGGAGTGAG
3181 -----+-----+-----+-----+-----+ 3240
CTCGACCCTTGGCTTCTCCCGTCACAGGATGTCGACTGACTTCGGAGGGCAACCTCACTC

a E L G T E E G S V L Q L T E A S R W S E -
AGCCTCTTGGAGGTGGTTCCAGACCCGGCCTATCCTCATCTCCCTGTGGATCCTCATAGGC
3241 -----+-----+-----+-----+-----+ 3300
TCGGAGAACCTCCACCAAGTCTGGGCCGATAGGAGTAGAGGGACACCTAGGAGTATCCG

a S L L E V V Q T R P I L I S L W I L I G -
AGTGTCTTGGGAGGGTGTCTCCTGCTTGTCTCTCTTGTCTTCTGCTGTGGAAGCTTGGC
3301 -----+-----+-----+-----+-----+ 3360
TCACAGGACCTCCCAACGAGGACGAACGAGAGGAACAGAAGACGGACACCTTCGAACCG

a S V L G G L L L L A L L V F C L W K L G -
TTCTTTGCCATAAGAAAATCCCTGAGGAAGAAAAAGAGAAGAGAAGTTGGAGCAATGA
3361 -----+-----+-----+-----+-----+ 3420
AAGAAACGGGTATTCTTTTAGGGACTCCTTCTTTTCTCTTCTTCAACCTCGTTACT

a F F A H K K I P E E E K R E E K L E Q
ATGTAGAATAAGGGTCTAGAAAGTCCCTGCGCAGCTTTCTTCAAGAGACTTGCATAAA
3421 -----+-----+-----+-----+-----+ 3480
TACATCTTATTCAGATCTTTCAGGAGGGACCGTCGAAAGAAGTCTCTGAACGTATT

AGCAGAGGTTTGGGGGCTCAGATGGGACAAGAAGCCGCTCTGGACTATCTCCCAGACC
3481 -----+-----+-----+-----+-----+ 3540
TCGTCTCCAAACCCCGAGTCTACCCTGTTCTTCGGCGGAGACCTGATAGAGGGGTCTGG

AGCAGCCTGACTTGACTTTTGTAGTCCTAGGGATGCTGCTGGCTAGAGATGAGGCTTTACC
3541 -----+-----+-----+-----+-----+ 3600
TCGTGGACTGAACTGAAACTCAGGATCCCTACGACGACCGATCTCTACTCCGAAATGG

TCAGACAAGAAGAGCTGGCACCAAACTAGCCATGCTCCACCCCTCTGCTTCCCTCCTCC
3601 -----+-----+-----+-----+-----+ 3660
AGTCTGTTCTTCTCGACCGTGGTTTGTATCGGTACGAGGGTGGGAGACGAAGGGAGGAGG

TCGTGATCCTGGTTCCATAGCCAACACTGGGGCTTTTGTGTTGGGGTCTTTTATCCCCAG
3661 -----+-----+-----+-----+-----+ 3720
AGCACTAGGACCAAGGTATCGGTTGTGACCCCGAAAAACAAACCCAGGAAAATAGGGGTC

GAATCAATAATTTTTTGCCTAGGAAAAAAAAGCGGCCGCAATTCGATATCAAGCT
3721 -----+-----+-----+-----+-----+ 3779
CTTAGTTATTAAAAAACGGATCCTTTTTTTTTCGCCGCGCTTAAGCTATAGTTTCGA

(2) INFORMATION FOR SEQ ID NO. 3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid and amino acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (iii) MOLECULAR TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: human
(B) CELLTYPE: chondrocyte
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO. 3:

```

      NdeI
      |
GGGGCATATGGTTTCAGAACCTGGGTTGCTACGTTGTTTCCGGTCTGATCATCTCCGCTCT
1  -----+-----+-----+-----+-----+ 60
CCCCGTATACCAAGTCTTGGACCCAACGATGCAACAAAGGCCAGACTAGTAGAGGCGAGA
b   G H M V Q N L G C Y V V S G L I I S A L -
    GTCGCCGGCTGTTGCTCACGGTGGTAACTACTTCCTAAGCTTGTCACAGGTATCAGCGG
61 -----+-----+-----+-----+-----+ 120
CGACGGCCGACAACGAGTGCCACCATTGATGAAGGATTGGAACAGGGTCCAATAGTCGCC
b   L P A V A H G G N Y F L S L S Q V I S G -
      BamHI
      |
CCTGGTGCCGCGCGGATCCCCC
121 -----+-----+-----+-----+ 143
GGACCAAGCGCGCCTAGGGGGG
b   L V P R G S P -
```

CLAIMS

1. A recombinant or isolated integrin subunit $\alpha 10$
5 comprising the amino acid sequence shown in SEQ ID No. 1
or SEQ ID No. 2, or homologues or fragments thereof hav-
ing similar biological activity.
2. A process of producing a recombinant integrin
subunit $\alpha 10$ comprising the amino acid sequence shown in
10 SEQ ID No. 1 or SEQ ID No. 2, or homologues or fragments
thereof having similar biological activity, which process
comprises the steps of
 - a) isolating a polynucleotide comprising a nucleo-
tide sequence coding for an integrin subunit $\alpha 10$, or
15 homologues or fragments thereof having similar biological
activity,
 - b) constructing an expression vector comprising the
isolated polynucleotide,
 - c) transforming a host cell with said expression
20 vector,
 - d) culturing said transformed host cell in a culture
medium under conditions suitable for expression of inte-
grin subunit $\alpha 10$, or homologues or fragments thereof hav-
ing similar biological activity, in said transformed host
25 cell, and, optionally,
 - e) isolating the integrin subunit $\alpha 10$, or homologues
or fragments thereof having similar biological activity,
from said transformed host cell or said culture medium.
3. A process of providing an integrin subunit $\alpha 10$,
30 or homologues or fragments thereof having similar biolo-
gical activity, whereby said subunit is isolated from a
cell in which it is naturally present.
4. An isolated polynucleotide comprising a nucleo-
tide coding for an integrin subunit $\alpha 10$, or for homo-
35 logues or fragments thereof, which polynucleotide comprises
the nucleotide sequence shown in SEQ ID No. 1 or SEQ ID
No. 2 or suitable parts thereof.

5. An isolated polynucleotide or oligonucleotide which hybridises to a DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof, wherein said polynucleotide or oligonucleotide fails to
5 hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$.

6. A vector comprising a polynucleotide or oligonucleotide coding for an integrin subunit $\alpha 10$, or homologues or fragments thereof, which polynucleotide or oligonucleotide comprises the nucleotide sequence shown in
10 SEQ ID No. 1 or SEQ ID No. 2 or parts thereof.

7. A vector comprising a polynucleotide or oligonucleotide which hybridises to a DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof,
15 wherein said polynucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$.

8. A cell containing the vector as defined in any one of claims 6 and 7.

9. A cell generated by the process in claim 2, in which a polynucleotide or oligonucleotide coding for an integrin subunit $\alpha 10$, or homologues or fragments thereof, which polynucleotide or oligonucleotide comprises the nucleotide sequence shown in SEQ ID No. 1 or SEQ ID No. 2
20 or parts thereof has been stably integrated in the cell genome.

10. Binding entities having the capability of binding specifically to integrin subunit $\alpha 10$ comprising the amino acid sequence of SEQ ID No. 1 or SEQ ID No. 2, or
30 to homologues or fragments thereof.

11. Binding entities according to claim 10, which are chosen from the group comprising proteins, peptides, carbohydrates, lipids, natural integrin binding ligands, polyclonal and monoclonal antibodies, and fragments
35 thereof.

12. A recombinant or isolated integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , in which the

subunit $\alpha 10$ comprises the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, and homologues and fragments thereof having similar biological activity.

13. A recombinant or isolated integrin heterodimer according to claim 12, wherein the subunit β is $\beta 1$.

14. A process of producing a recombinant integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , in which the subunit $\alpha 10$ comprises the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, and homologues and fragments thereof, which process comprises the steps of

a) isolating one polynucleotide comprising a nucleotide sequence coding for a subunit $\alpha 10$ of an integrin heterodimer and, optionally, another polynucleotide comprising a nucleotide sequence coding for a subunit β of an integrin heterodimer, or polynucleotides or oligonucleotides coding for homologues or fragments thereof having similar biological activity,

b) constructing an expression vector comprising said isolated polynucleotide coding for said subunit $\alpha 10$ optionally in combination with an expression vector comprising said isolated nucleotide coding for said subunit β ,

c) transforming a host cell with said expression vector or vectors,

d) culturing said transformed host cell in a culture medium under conditions suitable for expression of an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or homologues or fragments thereof having similar biological activity, in said transformed host cell, and, optionally,

e) isolating the integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or homologues or fragments thereof having similar biological activity, or the $\alpha 10$ subunit thereof from said transformed host cell or said culture medium.

15. A process of providing an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or homologues

or fragments thereof having similar biological activity, whereby said integrin heterodimer is isolated from a cell in which it is naturally present.

16. A cell containing a first vector, said first
5 vector comprising a polynucleotide or oligonucleotide coding for a subunit $\alpha 10$ of an integrin heterodimer, or for homologues or parts thereof having similar biological activity, which polynucleotide or oligonucleotide comprises the nucleotide sequence shown in SEQ ID No. 1 or
10 SEQ ID No. 2 or parts thereof, and a second vector, said second vector comprising a polynucleotide or oligonucleotide coding for a subunit β of an integrin heterodimer, or for homologues or fragments thereof.

17. Binding entities having the capability of bind-
15 ing specifically to the integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or to homologues or fragments thereof, or a subunit $\alpha 10$ thereof, having similar biological activity.

18. Binding entities according to claim 17, wherein
20 the subunit β is $\beta 1$.

19. Binding entities according to claim 17 or 18, which are chosen among the group comprising proteins, peptides, carbohydrates, lipids, natural integrin binding ligands, and fragments thereof.

20. A fragment of the integrin subunit $\alpha 10$, which
25 fragment is a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain.

21. A fragment according to claim 20, which is a
30 peptide comprising the amino acid sequence
KLGFFAHKKIPEEEKREEKLEQ.

22. A fragment according to claim 20, which comprises the amino acid sequence from about amino acid No. 952 to about amino acid no. 986 of SEQ ID No. 1.

23. A fragment according to claim 20, which is a
35 peptide comprising the amino acid sequence from about

amino acid No. 140 to about amino acid no. 337 of
SEQ ID No. 1.

24. A method of producing a fragment of the integrin subunit $\alpha 10$ as defined in any one of claims 20-23, which
5 method comprises a sequential addition of amino acids containing protective groups.

25. A polynucleotide or oligonucleotide coding for a fragment of the integrin subunit $\alpha 10$ as defined in any one of claims 20-23.

10 26. Binding entities having the capability of binding specifically to a fragment of the human integrin subunit $\alpha 10$ as defined in any one of claims 20-23.

27. Binding entities according to claim 26, which are chosen from the group comprising proteins, peptides,
15 carbohydrates, lipids, natural integrin binding ligands, and fragments thereof.

28. A process of using an integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or an integrin heterodimer comprising said
20 subunit $\alpha 10$ and a subunit β , or a homologue or fragment of said integrin or subunit having similar biological activity, as a marker or target molecule of cells or tissues expressing said integrin subunit $\alpha 10$, which cells or tissues are of animal including human origin.

25 29. A process according to claim 28, whereby said fragment is a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain.

30 30. A process according to claim 29, whereby said fragment is a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ.

31. A process according to claim 29, whereby said fragment comprises the amino acid sequence from about amino acid no. 952 to about amino acid no. 986 of
35 SEQ ID No. 1.

32. A process according to claim 29, whereby said fragment comprises the amino acid sequence from about

amino acid no. 140 to about amino acid no. 337 of
SEQ ID No. 1.

33. A process according to claim 28, whereby the
subunit β is $\beta 1$.

5 34. A process according to claim 28, whereby said
cells are chosen from the group comprising chondrocytes,
smooth muscle cells, endothelial cells, osteoblasts and
fibroblasts.

10 35. A process according to any one of claims 28-34,
which process is used during pathological conditions
involving said subunit $\alpha 10$.

36. A process according to claim 35, which patho-
logical conditions comprise damage of cartilage.

15 37. A process according to claim 36, which patho-
logical conditions comprise trauma, rheumatoid arthritis
and osteoarthritis.

38. A process according to any one of claims 28-34,
which is a process for detecting the formation of car-
tilage during embryonal development.

20 39. A process according to any one of claims 28-34,
which is a process for detecting physiological or thera-
peutic reparation of cartilage.

40. A process according to any one of claims 28-34,
which is a process for selection and analysis, or for
25 sorting, isolating or purification of chondrocytes.

41. A process according to any one of claims 28-34,
which is a process for detecting regeneration of carti-
lage or chondrocytes during transplantation of cartilage
or chondrocytes.

30 42. A process according to any one of claims 28-34,
which is a process for in vitro studies of differentia-
tion of chondrocytes.

43. A process of using binding entities having the
capability of binding specifically to an integrin subunit
35 $\alpha 10$ comprising the amino acid sequence shown in SEQ ID
No. 1 or SEQ ID No. 2, or an integrin heterodimer com-
prising said subunit $\alpha 10$ and a subunit β , or to homo-

logues or fragments thereof having similar biological activity, as markers or target molecules of cells or tissues expressing said integrin subunit $\alpha 10$, which cells or tissues are of animal including human origin.

5 44. A process according to claim 43, whereby said fragment is a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain.

10 45. A process according to claim 43, whereby said fragment is a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ.

15 46. A process according to claim 43, whereby said fragment comprises the amino acid sequence from about amino acid no. 952 to about amino acid no. 986 of SEQ ID No. 1.

20 47. A process according to claim 43, whereby said fragment comprises the amino acid sequence from about amino acid no. 140 to about amino acid No. 337 of SEQ ID No. 1.

20 48. A process according to claim 43, whereby the subunit β is $\beta 1$.

25 49. A process according to any one of claims 43-48, which is a process for detecting the presence of an integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID No. 1 or SEQ ID No. 2, or of an integrin heterodimer comprising said subunit $\alpha 10$ and a subunit β , or of homologues or fragments thereof having similar biological activity.

30 50. A process according to any one of claims 43-48, which process is a process for determining the differentiation-state of cells during embryonic development, angiogenesis, or development of cancer.

35 51. A process for detecting the presence of an integrin subunit $\alpha 10$, or of a homologue or fragment of said integrin subunit having similar biological activity, on cells, whereby a polynucleotide or oligonucleotide chosen from the group comprising a polynucleotide or oligo-

nucleotide shown in SEQ ID No. 1 is used as a marker under hybridisation conditions wherein said polynucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$.

5 52. A process according to claim 51, whereby said cells are chosen from the group comprising chondrocytes, smooth muscle cells, endothelial cells, osteoblasts and fibroblasts.

10 53. A process according to claim 51, whereby said fragment is a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain.

15 54. A process according to claim 53, whereby said fragment is a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ.

55. A process according to claim 53, whereby said fragment comprises the amino acid sequence from about amino acid No. 952 to about amino acid no. 986 of SEQ ID No. 1.

20 56. A process according to claim 53, whereby said fragment comprises the amino acid sequence from about amino acid No. 140 to about amino acid No. 337 of SEQ ID No. 1.

25 57. A process according to any one of claims 43-48, which is a process for determining the differentiation-state of cells during development, in pathological conditions, in tissue regeneration or in therapeutic and physiological repair of cartilage.

30 58. A process according to claim 57, wherein the pathological conditions are any pathological conditions involving the integrin subunit $\alpha 10$.

59. A process according to claim 58, whereby said pathological conditions are rheumatoid arthritis, osteoarthritis or cancer.

35 60. A process according to claim 57, whereby said cells are chosen from the group comprising chondrocytes,

smooth muscle cells, endothelial cells, osteoblasts and fibroblasts.

61. A process for determining the differentiation-state of cells during development, in pathological conditions, in tissue regeneration and in therapeutic and physiological reparation of cartilage, whereby a polynucleotide or oligonucleotide chosen from the nucleotide sequence shown in SEQ ID No. 1 is used as a marker under hybridisation conditions wherein said polynucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$.

62. A process according to claim 61, whereby said polynucleotide or oligonucleotide is a polynucleotide or oligonucleotide coding for a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the spliced domain.

63. A process according to claim 62, whereby said polynucleotide or oligonucleotide is a polynucleotide or oligonucleotide coding for a peptide comprising the amino acid sequence KLGFFAHKKIPEEEKREEKLEQ.

64. A process according to claim 62, whereby said peptide comprises the amino acid sequence from about amino acid no. 952 to about amino acid no. 986 of SEQ ID No. 1.

65. A process according to claim 62, whereby said peptide comprises the amino acid sequence from about amino acid no. 140 to about amino acid no. 337 of SEQ ID No. 1.

66. A process according to claim 61, whereby said pathological conditions are any pathological conditions involving the integrin subunit $\alpha 10$.

67. A process according to claim 66, whereby said pathological conditions are rheumatoid arthritis, osteoarthritis or cancer.

68. A process according to claim 66, whereby said pathological conditions are atherosclerosis or inflammation.

69. A process according to any one of claims 61-68, whereby said cells are chosen from the group comprising chondrocytes, smooth muscle cells, endothelial cells, osteoblasts and fibroblasts.

5 70. A pharmaceutical composition comprising as an active ingredient a pharmaceutical agent or an antibody which is capable of using an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or
10 subunit $\alpha 10$ having similar biological activity, as a target molecule.

 71. A pharmaceutical composition according to claim 70, for use in stimulating, inhibiting or blocking the formation of cartilage, bone or blood vessels.

15 72. A pharmaceutical composition according to claim 70, for use in preventing adhesion between tendon/ligaments and the surrounding tissue after infection, inflammation and after surgical intervention where adhesion impairs the function of the tissue.

20 73. A vaccine comprising as an active ingredient an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$, or DNA or RNA coding for said integrin subunit $\alpha 10$.

25 74. Use of the integrin subunit $\alpha 10$ as a marker or target in transplantation of cartilage or chondrocytes.

 75. A method of using binding entities having the capability of binding specifically to an integrin subunit $\alpha 10$ comprising the amino acid sequence shown in SEQ ID
30 No. 1 or SEQ ID No. 2, or an integrin heterodimer comprising said subunit $\alpha 10$ and a subunit β , or to homologues or fragments thereof having similar biological activity, for promoting adhesion of chondrocytes and/or osteoblasts to surfaces of implants to stimulate osseo-
35 integration.

 76. Use of an integrin heterodimer comprising an integrin subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$

thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity, as a target for anti-adhesive drugs or molecules in tendon, ligament, skeletal muscle or other tissues where adhesion
5 impairs the function of the tissue.

77. A method of stimulating, inhibiting or blocking the formation of cartilage or bone, comprising administration to a subject a suitable amount of a pharmaceutical agent or an antibody which is capable of using an
10 integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity, as a target molecule.

78. A method of preventing adhesion between tendon/
15 ligaments and the surrounding tissue after infection, inflammation and after surgical intervention where adhesion impairs the function of the tissue, comprising administration to a subject a suitable amount of a pharmaceutical agent or an antibody which is capable of using a
20 integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity, as a target molecule.

79. A method of stimulating extracellular matrix
25 synthesis and repair by activation or blockage of an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or of the subunit $\alpha 10$ thereof, or of a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity.

80. A method of in vitro detecting the presence of
30 integrin binding entities, comprising interaction of an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit, with a sample,
35 thereby causing said integrin, subunit $\alpha 10$, or homologue or fragment thereof having similar biological activity,

to modulate the binding to its natural ligand or other integrin binding proteins present in said sample.

81. A method of in vitro studying consequences of the interaction of a human heterodimer integrin comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit, with an integrin binding entity and thereby initiate a cellular reaction.

82. A method according to claim 81, whereby the consequences of said interactions are measured as alterations in cellular functions.

83. A method of using DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof as a target molecule.

84. A method according to claim 83, whereby a polynucleotide or oligonucleotide hybridises to the DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof and whereby said polynucleotide or oligonucleotide fails to hybridise to a DNA or RNA encoding an integrin subunit $\alpha 1$.

85. A method of using a human heterodimer integrin comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit, or a DNA or RNA encoding an integrin subunit $\alpha 10$ or homologues or fragments thereof, as a marker or target molecule during angiogenesis.

86. A pharmaceutical composition comprising as an active ingredient a pharmaceutical agent or an antibody which is capable of stimulating cell surface expression of an integrin heterodimer comprising a subunit $\alpha 10$ and a subunit β , or the subunit $\alpha 10$ thereof, or a homologue or fragment of said integrin or subunit $\alpha 10$ having similar biological activity.

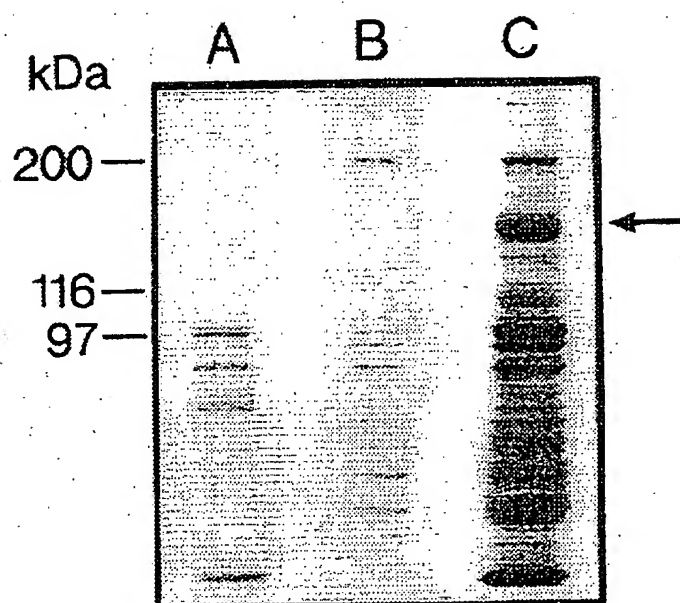


FIGURE 1

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Peptide	Amino acid sequence
1	DNTAQTSAYIQYEPHHSI
2	GPGHWDR
3	AAFDGSGQR
4	FAMGALPD
5	FTASLDEWTTAAR
6	VDASFRPQGXLAP

FIGURE 2

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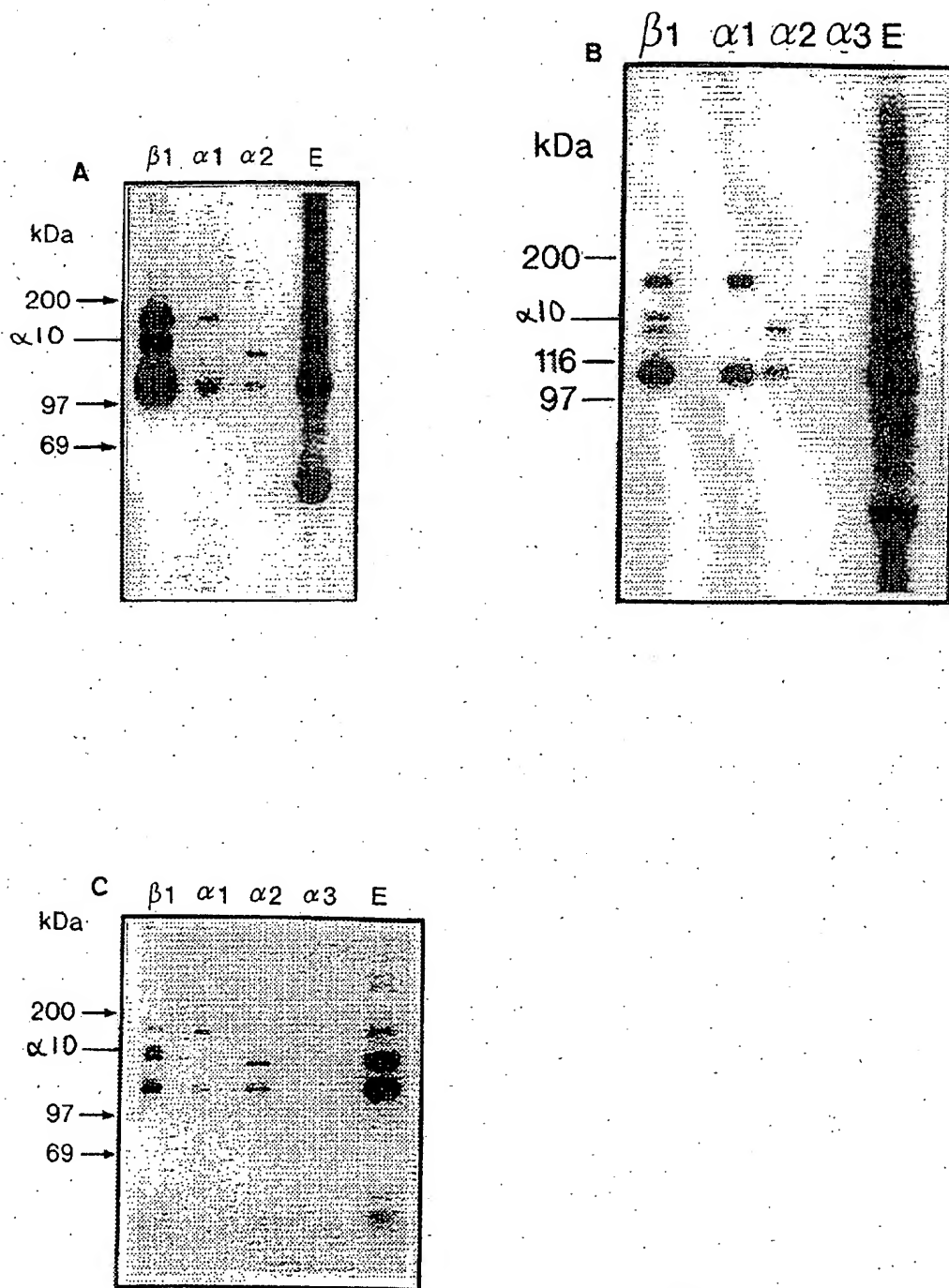


FIGURE 3

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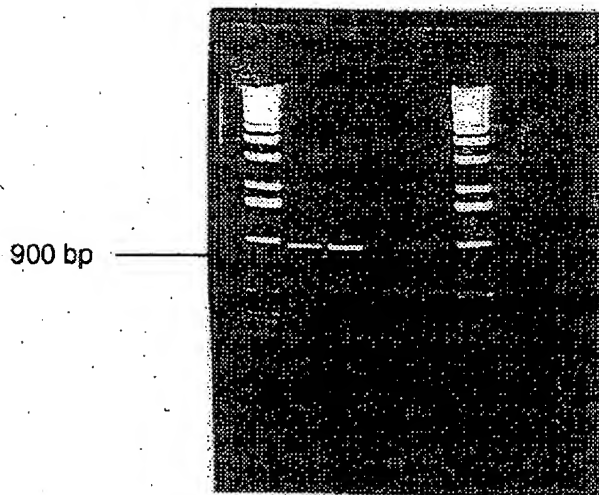


FIGURE 4

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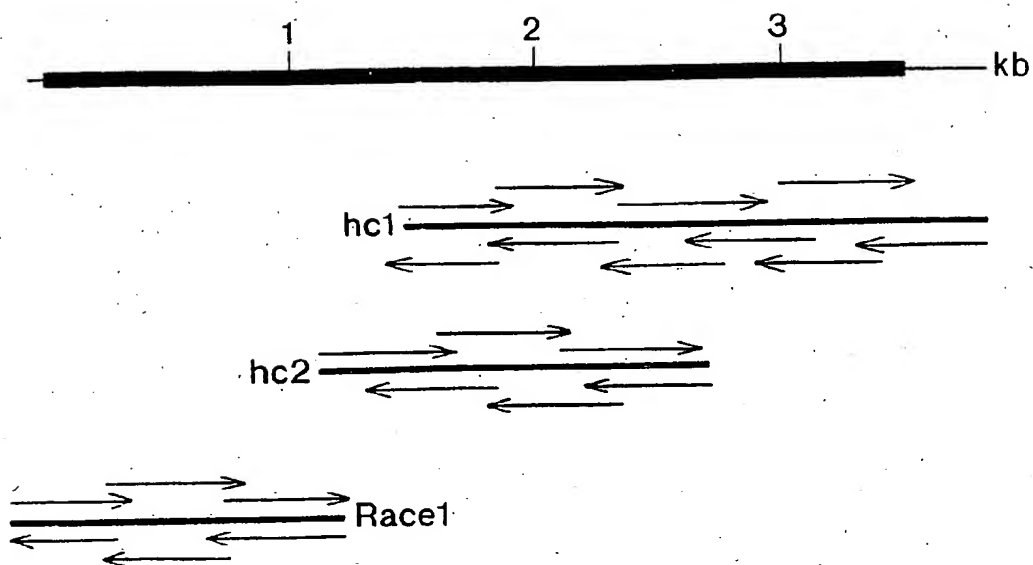


FIGURE 5

SUBSTITUTE SHEET (RULE 26)

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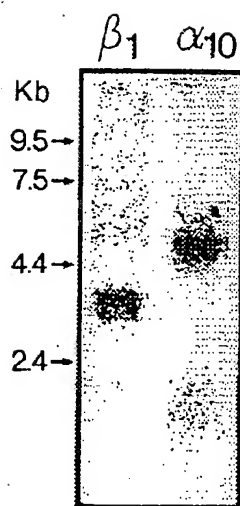
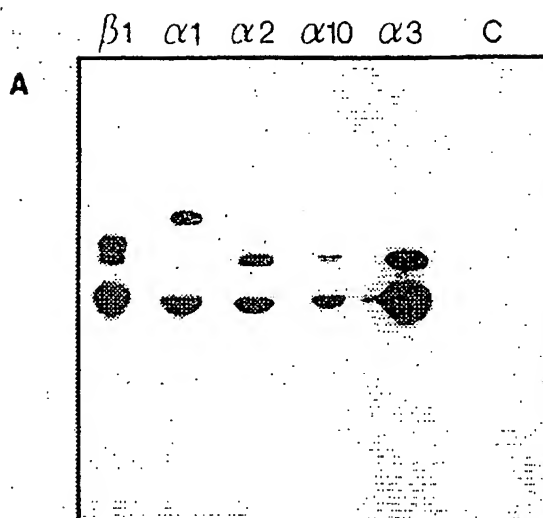


FIGURE 7

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B IP: $\alpha 10$ $\beta 1$
 Blot: $\beta 1$ $\beta 1$

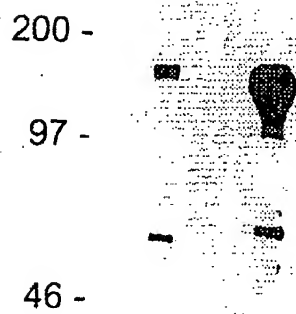


FIGURE 8

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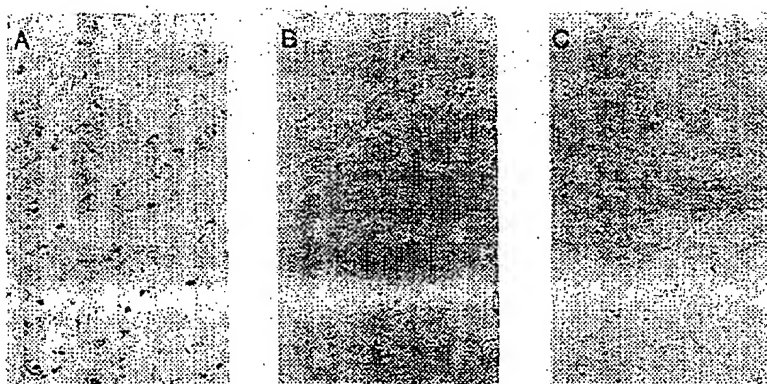


FIGURE 9

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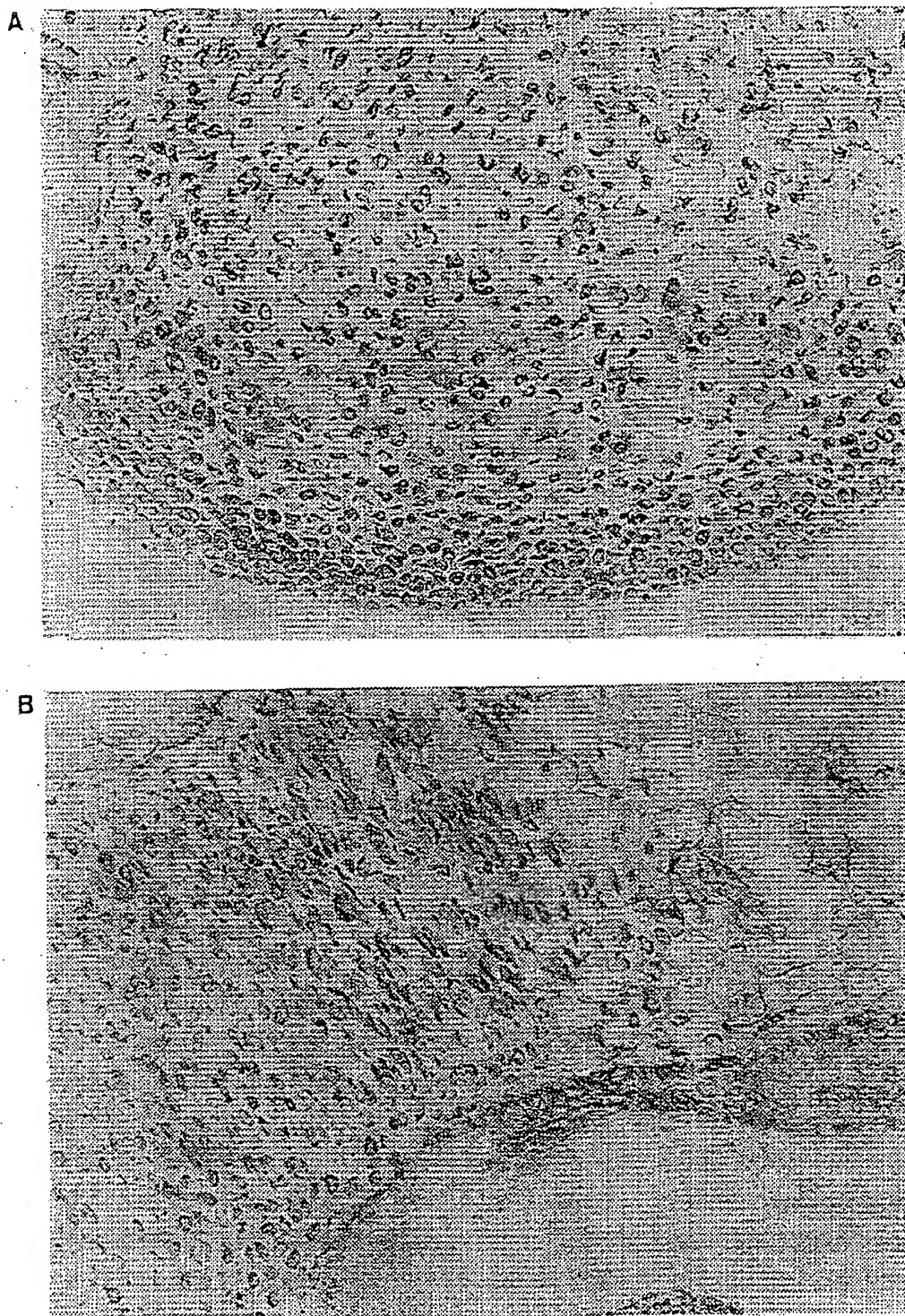
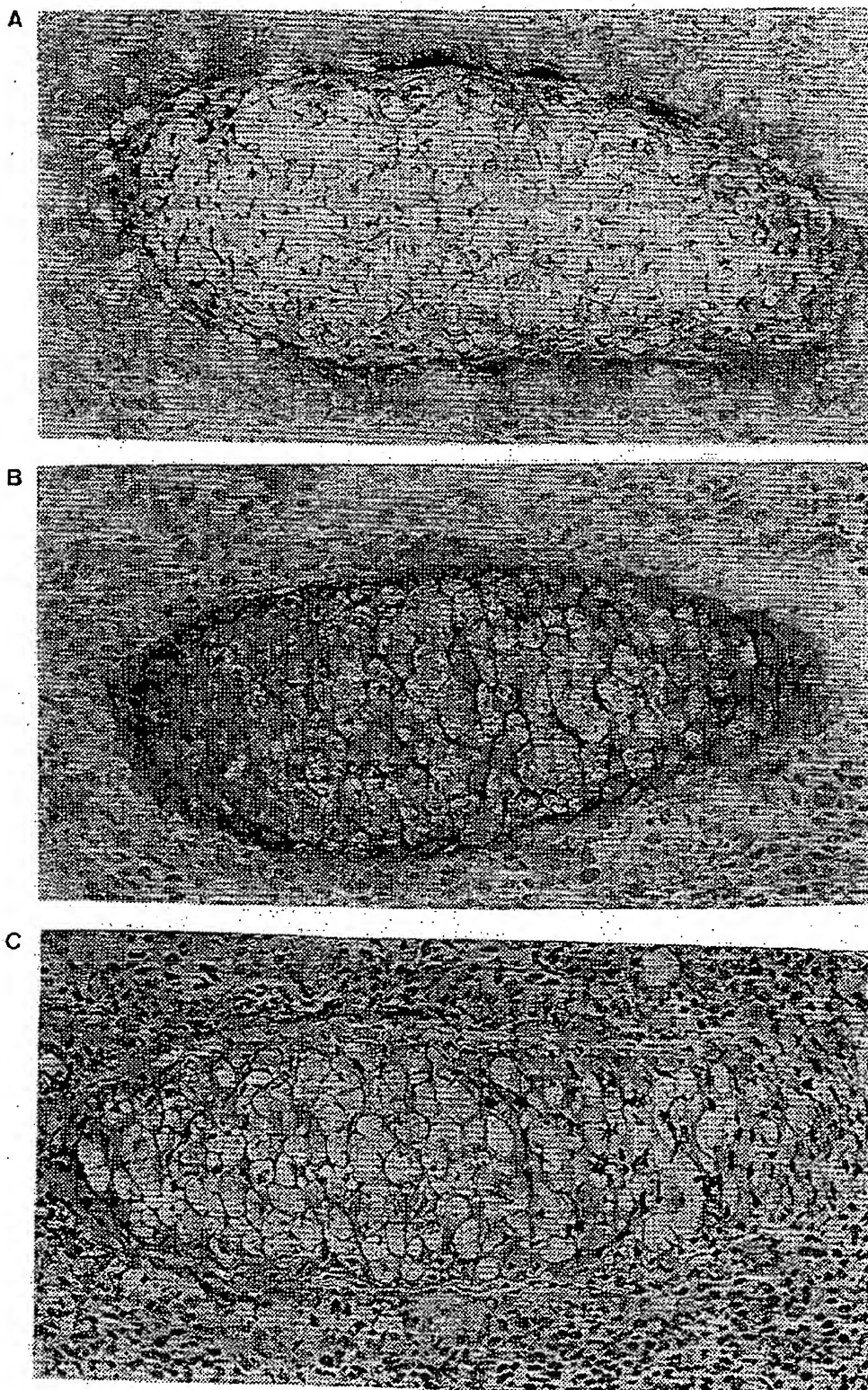


FIGURE 10

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Human RNA Master blot

Tissue	$\alpha 10$ expression	Tissue	$\alpha 10$ expression
Aorta	++++	Thyroid gland	-
Trachea	+	Salivary gland	-
Lung	++	Spleen	-
Fetal lung	++	Fetal spleen	-
Kidney	++	Thymus	-
Fetal kidney	(+)	Fetal thymus	-
Heart	(+)	Peripheral leucocyte	-
Fetal heart	++	Lymph node	-
Spinal cord	++	Appendix	-
Mammary gland	(+)	Placenta	-
Bone marrow	(+)	Whole brain	-
Small intestine	(+)	Fetal brain	-
Skeletal muscle	-	Amygdala	-
Liver	-	Caudate nucleus	-
Fetal liver	-	Cerebellum	-
Colon	-	Cerebral cortex	-
Bladder	-	Frontal lobe	-
Uterus	-	Hippocampus	-
Prostate	-	Medulla oblongata	-
Stomach	-	Occipital lobe	-
Testis	-	Putamen	-
Ovary	-	Substantia nigra	-
Pancreas	-	Temporal lobe	-
Pituitary gland	-	Thalamus	-
Adrenal gland	-	Subthalamic nucleus	-

FIGURE 12

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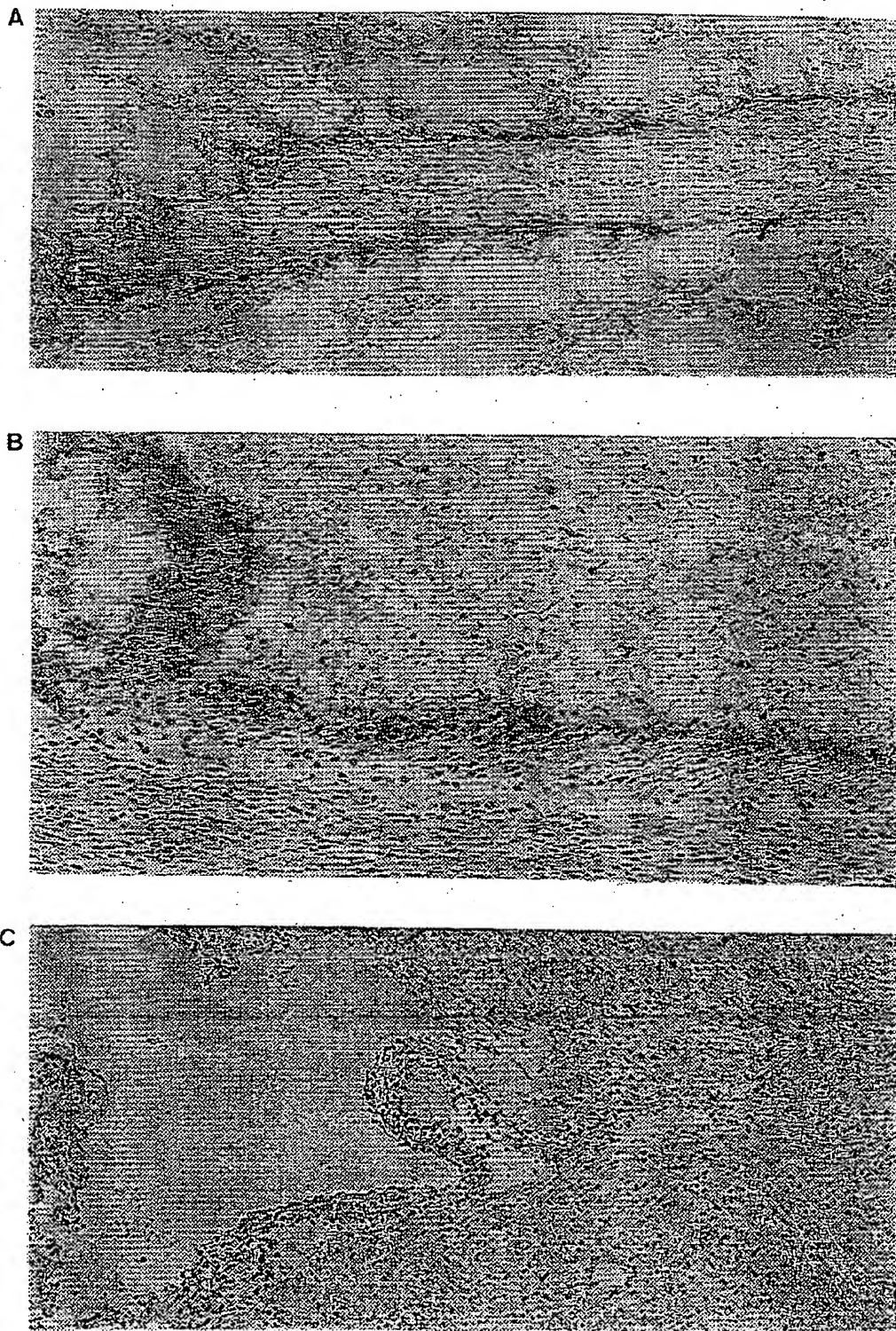


FIGURE 13

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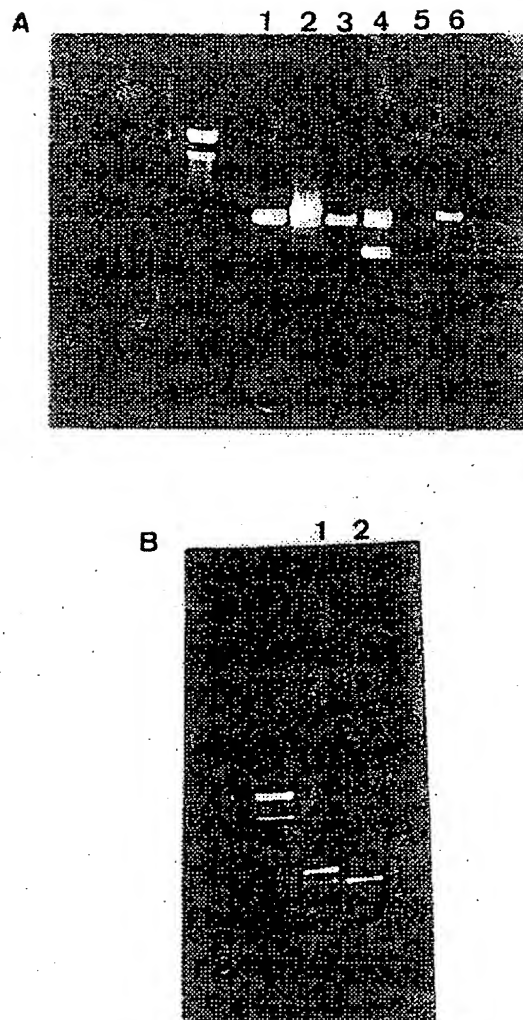


FIGURE 14

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TGNTTHKKKCHCAGGAKHCHWSAKGNCCGAKGGTGKGVAAVGTGACARAGCTNGHNAARANGAAGTATGACCMGTGCCC 80
? ? ? ? R ? ? ? P ? ? ? V ? ? ? D ? ? ? A ? ? ? K ? ? ? K Y D ? ? W A
? ? ? ? H ? ? ? ? ? R ? ? ? ? ? V ? ? ? L ? ? ? K ? ? ? S M T ? ? G
V ? ? ? ? T ? ? ? ? ? G ? ? ? ? ? . Q S ? ? ? K ? ? ? E V . . P V G
CRAGATAGHKAMDAAGCNGHSAGKTRAMGGACGATGGNCCGCGCAAVOGABWGGNAHTBCGGCNWDCARNGTCCAAATK 160
? ? ? ? K ? ? ? ? ? G R W ? ? ? Q ? ? ? G ? ? ? G ? ? ? Q ? ? ? P N
P R ? ? ? S ? ? ? ? ? D D G P A ? ? ? R ? ? ? ? ? A ? ? ? ? ? V Q ?
? ? ? ? A ? ? ? ? ? R T M ? ? ? P ? ? ? ? ? ? ? R ? ? ? ? ? V K ?
SANKTCS CAGGAACCMACCGANTGGCTCGCARCCCTAGGGATCAGGKACGATGRCCTSCCGRNSKACTCSGNKTGATWA 240
? ? ? ? R N ? ? ? ? G S Q P ? ? ? I R ? ? ? D ? ? ? S P ? ? ? S ? ? ?
? ? ? ? G T ? ? ? A R ? ? ? . G S G T M ? ? ? R ? ? ? T ? ? ? T ? ? ?
? ? ? ? S Q E P T ? ? ? W L A ? ? ? R D Q ? ? ? R ? ? ? L ? ? ? ? ? L ? ? ? I
ATCGHNGTGHGAGCGCGHGAATTHAAAGTANTGGTHGAMAKATGNGVHGGAHATCATRRGTMGACTVTHVNGGVAK 320
I ? ? ? R ? ? ? A ? ? ? E L ? ? ? S ? ? ? G R ? ? ? M ? ? ? R ? ? ? . ? ? ? V D ? ? ? ? ? G ?
S ? ? ? V G R R R R N ? ? ? K V ? ? ? V ? ? ? ? ? ? ? G ? ? ? D ? ? ? ? ? T ? ? ? ? ?
N R ? ? ? ? ? G G G I ? ? ? X ? ? ? W ? ? ? ? ? ? ? ? ? ? ? M ? ? ? ? ? R L ? ? ? ? ? R ?
VTAKSGGTACAGCGCAAKACARGAKGTGTCTGAGGAADTCAGNAGGACAAHMTGCCGAAGTCHGGACTTAGKATRGAT 400
? ? ? ? Y R R ? ? ? Q ? ? ? V . G ? ? ? Q ? ? ? D ? ? ? A E V R T . ? ? ?
? ? ? ? G T G E ? ? ? ? ? V S E E ? ? ? R T ? ? ? L P K S Q L ? ? ? ? ? D
? ? ? ? V Q A ? ? ? ? ? C L R ? ? ? S ? ? ? G Q ? ? ? C R S ? ? ? D L ? ? ? ? ? I
ACGAANCKTRGATCTTAHAGGGGGGNKAGCGAGTGCSTAAACGVARATRGONSWGCTCTACTTMAACNCCAAGNGDGGACA 480
Y E ? ? ? I L ? ? ? G G ? ? ? R V ? ? ? K R ? ? ? ? ? ? ? L L ? ? ? ? ? Q ? ? ? ? ? T
T ? ? ? ? S ? ? ? ? ? G ? ? ? S E C ? ? ? N ? ? ? ? ? ? ? V Y ? ? ? N ? ? ? K ? ? ? G H
R ? ? ? ? D L ? ? ? ? ? G ? ? ? A S A . T ? ? ? ? G ? ? ? S T ? ? ? T P ? ? ? ? ? D
TTTACTAGAGGAGAGAGTAGCCAGATCACDTGAGATGATCTAAKGTGGGGTCCCGTTGCCAGTATATGAGAGGACTGGT 560
F T R ? ? ? G E . P D H ? ? ? R . S ? ? ? V G S R C Q Y M R G L V
L L ? ? ? E E S S Q I T . D D L ? ? ? W G P V A S I . E D W
I Y . ? ? R R V A R S ? ? ? E M I . ? ? G V P L P V Y E R T G
TGGCAGACATGATGCTCTTTGCTGACTCACATATTGTTGCCVTGAGKATGATCAGATACGATCTGNTGTCCTCATCA 640
R Q T ? ? ? M L F A D S H I V A ? ? ? M I R Y D L ? ? ? S L I
P R H ? ? ? C S L L T H I L L P . ? ? ? S D T I ? ? ? C P S S
S A D I D A L C . L T Y C C ? ? ? E ? ? ? D Q I R S ? ? ? V P H H
TGAATSTGRGCGTCACTGTAATGAGATTCCCTATGATGGAACAAGAGACTTHTGCTACAGCAGCGAATGAAGGTTTC 720
M N ? ? ? R D A N E I R L . W N K R L ? ? ? L Q Q A N E G F
? ? ? ? A V M L M R F A Y D G T R D ? ? ? C Y S R R M K V S
E ? ? ? P . C . . D S P M M E Q E T ? ? ? A T A G E . R F
TAGAGTAGGAGTCTCAGGAGGAGAGAACTGTGGACCTGGAGGACCAGGGACTCCAGGAGGAAGTWCCACAACTGGCTT 800
S R S L R R R R E T V D L E D Q G L Q E E V A T T G L
R V G V S G G E K L W T W R T R D S R R K ? ? ? P O L A
L E . E S Q E E R N C G P G G P G T P G G S ? ? ? H N W L
GMAGTTTGGGCTCCGATCTGATACAGGCTGCTGCTTGGAGTTATCCCTCTCTTGTGATGGCTCAGAAATGCTCTG 880
? ? ? R L R S . Y ? ? ? L V L ? ? ? V I P L S C W M A O K R L
? ? ? S G S D P D T G S S ? ? ? E L S P S L A G W L R N A W
? ? ? S A P I L I ? ? ? A R P ? ? ? S Y P P L L L L D G S E M P G
ACCTTTTCATCCCACTGGACAAACTAGGCGTCTGCGCTTGTGCGCTGGGATTGTGGGGCTGTGTGGCTCATATCTC 960
D L F I P T G Q T R R L A L W P W D C G A V W P H I L
T F S S P L D K L G V W R C G P G I V G L C G L I S
P F H P H W T N . A S G V V A L G L W G C V A S Y P
CATTCGTCTATTCTCACCTAATCTGTCCCTGGNTACGACTCAAGCCCYGACTGACANTGTGTTACAGATAGGAGGG 1040
H S V Y S H P N L S L ? ? ? T T Q A ? ? ? T D ? ? ? V V Q D K E G
I L S I L T L I C P W ? ? ? R L K P ? ? ? L T ? ? ? W Y K I R R
P F C L F S P . S V P G Y D S S P D . ? ? ? C G T R . G G
AGCCAGGTGGGTGAGATGGAAGCTGAGATGGTNCAGTGTGTCGACCTCATTGTAATTCAACTNCTTGAGTGAAGTT 1120
A O V G E M R A E M V H C V P T S L . F N ? ? ? L D . S
E P R W V R W K L R W ? ? ? T V C ? ? ? P H C N S T ? ? ? L T E V
S P O G . D G S . D G ? ? ? L C A ? ? ? L I V I Q L P . L K L
AAAAATCCAGATCCYTAGGGATGAGGGGAAGAACCTGCCAAGACGGGTGAGGAAGGAGTGTCTAAGGGAAGGCTCTGCA 1200
N P D P . G . G E E P A K D G S G R Q C . G K A P A
K I Q I ? ? ? R D E C K N L P K T G Q E G S A K G R L L Q
K S R S L G M R G R T C Q R R V R K A V L R E G S C
GGCCTCTGCACTTGGACTTCATTGAGTCCCATGCGCAATCTCATAGCTCTTCCCTTATCTCTCTGTCTTGAGTCTAG 1280
G L S A V G L H S V P L A R I S . L F P L S L C L E S S
R P L Q L D F I Q S H C O N L I A L P ? ? ? I S L S . V .
TTAAGAAATTTGTTACCGAGACAGAATCTCTTTCTTAGCCTCCTGCGCAGATATTTAAAGGAGGGGGTGGGTACTT 1360
E P V T G D R I L F L S L L A R Y L K G G C W V T
V K H L L F S T E F S F L A S W P D I . K E G G G L L
L R I C Y R R Q N S L S . P P G Q I F K R R G V G Y F

FIGURE 15a

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TTTGGTAAGGGAAGCTTAAGTTATGGATAGCAAAGTGCTAATTGTATCTTTTTTCTGAAACCTCATGTAGCATTTTTTC 1440
FW . G K L K L W I A K C . L Y S F F L K P H V A F F
F G A G S L S Y G . Q S A N C I L P P . N L H . H F S
L V G E A . V N D S K V L I V F F F S E T S C S I F
TTCCCTTCACCCCTCCATACTTTCCAGGCTTCATTTTCATGCCCGGCTCTCTTCGCTCACACCGCTGACAGGTGTGTA 1520
F P S T L H T F P G F I S C P A S L R S H R C R L F E
S . L P P S I L S Q A S F H A R R L F A H T A A G C L
L P F H P P Y F P R L H F M P G V S S L T P L Q A V .
GGCTTCTCCCTGGGTCTGGCTCAGCAGACTGGCTCCACACTTTCAGTTCCTGGGTACAGCTTGATATTAGAGTTTCT 1600
A S P L G L P Q Q T A S T L S S F C V H V D I R V S
R L L P W V C L S R L P P M F P V S A Y T L I L E F F
G F S P G S A S A D C L H T F Q F L R T R . Y . S F L
TCCCCACTTGGCTTGTCTTCTCTGACTACCCAGGCTGATGCCATGCTGGGCTCTTCTGTAAATACTGTACAAATG 1680
F P T W L L L F L . L P R L M F C L A S S C K Y C T H
S P L G S C S F S D Y P G . C H V W P L P V N T V Q .
P H L A L A L S L T T Q A D A M S G L F L . I L Y N
ATTCTATGTAATAACTGGTCTTGGCCACAGACAAGCAAGCCTTCTAGGCTAACAAATTAAGATCAAGTTTGTCTCAC 1760
I L C K . L V L A H R A S K P S R L T N . R S S L L T
F Y V N N W S L P T E O A S L L O . Q I K D Q V C S
D S H . I T G F C P Q S K Q A F . A N K L K I K F A H
TGACTTTTATTCAATCAAGATGCGGGGGTGGGGTGGGGGGCGGATTGCGCTTTTCACTGTGGTACCTAGGCGAG 1840
D F F I Q F K M A G G G V G G R I A C F H C G T . A
L T F L F N S R W R G V G W G G G L P V F T V V P R Q
L F Y S I Q D G G G W G G G A D C L F S L W Y L G R
GGCTGAAGCTCTGAGCTCCCTGCTTCTAGGCTCTGAGTAGCTACAGTGAAGTGTACTGTGTCCAGCTCTGCTTGACA 1920
G L K L . A P L L . A S E . P T V S V T V S S C S L T
G . S S S L P C F R L L S S L Q . V L L C P A A R . H
A E A L S S P A L G F . V A Y S E C Y C V Q L L V D
TCTGGTCTCTCATGGTCTGGTCAATGTAAGCCTTAGCTCTCTGACTGTGGATGGCTTCTCTGGGTTAGCAGTAAACAT 2000
S G L S W S G H C K P . L S D C O W L S L A L A A N H
L V S H G L V I V S L S L T V D G F P W R . O L T
I W S L H V W S L . A L A L . L W M A F L G V S S . H
GGTTACAGGATTTCACTGAAATTTAAATGTTGGGGGAAAGGTGCGGACACACCATTAATGGTCCCAATTCAAAACATCC 2080
V T G F H . K F K C W G K G A D T P . W S Q F K T I
W L Q D F T E N G G K V R T H N H G P N S K Q S
G Y R I S L K I . M L G E R C G H T I M V P I Q N N P
GTGAACAGCTCAAGTTAGGGGTGAGATGTTTCAACCAAAGTAATTATCTTGACACCAACAAAGCACACCTGTCTACAG 2160
R E T A S S . G . D V F N Q S N Y L D T T K H T C L Q
V K O P Q V R G S H F S T K V I I L T P Q S T P V Y R
N S L K L G V R C F O P K . L S . H H K A H L S T
GCAGTGACTCCCCAAAGCTATTAGACACACAAGCATGACCATAACTCAGTGGATTGGCAAGGTCACAGTAGGAC 2240
A V T P Q K L L D T Q Q A . P . L S G L A R S H S R T
Q . L P K S Y . T H N K H D H N S V D W O G H T V G
Q S D S P K A I R H T T S M T I T O W I G K V T Q . D
TGCCCTTCACACAGTAGGTAGGAAAATGCTGCTGTCACTGCTGTCACTGTTTATTTTGCATATCCCATGTTAAGATTAA 2320
A L H T V G R K M L L S L S A V I L H I P C . D .
L F F T O . V G K C C C H C C O L L F C I S H V K I N
C P S H S R . E N A A V T A V S C Y F A Y P M L R L I
AAGGCAAAAATATTGTCTTAAGTCTACTTTCTGTTCCAACTGGAGGAAATATTGAATAAATAAACCGTGCATAAA 2400
G K K Y C L . V L L S V P N W R K L L N K . T V N K
K A K N I V S K S Y F L F O T G G N Y . I N K P C I K
R Q K I L S L S P T F C S K L E E I T E . I N R A .
AGTAGCCTCAGAAAGGCTCAAAATTTGTGTTTCTTTGAATATTAGCTGAGGCTCCAGGGGGCAGCACCAGGTAGAGA 2480
S S L R K G O N L C F L . I L A E A S R C Q H Q G R E
V A S E R V K I C V F F E Y . L R P P G G S T K V R E
K . P Q K G S K F V F S L N I S . G L Q G A A P R . R
CGTGACTAAGGCTCTGTGTTCTGCTGCTGGGCTCCCCACAGCTCCCTCCACCAGCCTCCCATTCATCCCACTT 2560
L D . G C S V F L S W A P H S S L P P P L F F H P T
S W T K A A L C S C P G L P T A P F H H S H S I O L
A G L R L L C V P V L G S P Q L P S T T T P I F S N F
TATTTTTAGCTGCGAGTGGAGGGGGCAGGATAGGAGGAAAGTAAGCAAAACAGCCAGGAGAGGACAGMICAATCA 2640
L F L A A S G R G Q D R R E S N E N S Q G E G Q S N S
I F S C O W E G A G . E G K . R K O P R R R G T E Q L
GAGCCTCTCGGACTGGACCGGACAAGCGCCCTGAGTCTCTCTCCATCCCTCACCTGCTGCTGCCCCGGCGTGWGCTGA 2720
E P L G L D R T S A H G V S L H P S P A P A P A P G V A D
S L S D W T G Q A P H E S L S I P H L L L L P L A T L
R A S R T G P D K R P W S L S S L T C S C P W R 7 .

FIGURE 15b

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CAGGTGAGGGAAGCAAACCTTGGTTTCTGCTGGGAATGGAAGTTATGTGGATTGTTTATAATTGGGACCATTATGGCTAAA 2900
R . G K Q T W F L L G M E V M W I V Y N W D H Y G .
I C E C S X L G F C W E W K L C G L F I I G T I M A K
Q V R E A N L V S A G N G S Y V D C L . L G P L W L K
ATCTYGGGGCGCTCAGGTCCGAGGTTAATACCGATGCTATATTTCCTGTGTGCACTCATGTTCTTAGACACCCAAATGG 2880
N L A G A Q V G G . Y R C Y I S C V H S C S . T P K W
I ? R A L R S E V N T D A I F P V C T H V L R H P N G
S ? G R S G R R L I P M L Y F L C A L M F L D T Q M
CAGTGGCCAAAACCTTCTCTGGCTTGTACCTCATTATCTAAAGCTTTGTACCTAATTATCTAAACCTTGGTCTTAAACT 2960
Q W P K L P L A C T S L S K P L Y L I . N L G P K L
S G Q N F L W L V P H Y L N L C T . L S K T L V L N
A V A K T S S G L Y L I . T F V P N Y L K P W S . T
CCACAGACATGAGGGCAGAGAAAGAGACGTGTCTCATCTTCCATTCCGTTACACTGATTCTACCTTCCCTGCTTCT 3040
H R H E G T E K R R V S H L P F G Y T D S Y L P C F
S T D M R A Q K R D V S L I P H S V T L I P T F P A S
P Q T . G H R K E T C L S S S I R L H . F L P S L L L
CCCTGCCATTGGTGCTCCTTGGTGCTGAGGCATAATTCCTTACTATGTGCTCAGAACTCTGGGTTCCGCTAACGACC 3120
S L P L V L L G A . G I I A L L C G Q N S G F A . R P
P C H W C S L V P E A . L P Y V V V R T L G S P N D R
P A I G A P W C L R H N C L T M W S E L W V R L T T
AGCTACAGTTTCTGGTCTCATAGCCCTGCCAATTTCTGGATTAAAAAAGGCTCACATATAAAATACCTTTTCTGA 3200
S Y S F W S H S P A N F L D . K K K A H I . N T F S E
A T V S G L I A L P I S W I K K K R L T Y K I P F L
E L Q F L V S . P C Q F P O L K K K G S H I K Y L F .
AAATGAGCAGAGTGTGAGTTGAAGTTAGATTTTGGGGATGAGGGTGTCTTGGATGCCAAGAGCAAGACAGTAGAGAAG 3280
N E H S V S . S . I L G D G G L L G C K E Q D S R E
K M S T V . V E V R E W G M E G C L D A K S K T V E K
K . A O C E L K L D F G G W R V A W M Q R A R Q . R R
AGAATCATGGGAGGATAAGAGGCTGGAATTTTCCCTGCTAGTGCCCTATAATCTTTGTTTCTAAAATAACAGCTCTG 3360
E N H G R D K R L E F F P A S A L . S L P P K I T A L
R I M G G I R G W N F S L L V P Y N L C F L K . Q L
E S W E G . E A G I F P C . C P I I F V S . N N S
ATTTTATGGGAATTTGGGCTCAGGAGAAAGGAATCAGTAGGCACAGATGGGACCCCAAGCGTGAGCTAAAGTTTGAGGAAA 3440
I L W E L G S G E R N O . A O M G P Q A W T K V . G N
F Y G N W G Q E K G I S R H R W D P K R G L K F E E
D F M G I G V R R K E S V Q T D G T P S V D . S L R K
CTATGGGAGTAGCAAGGGGTGTTTGTAGGTGATGAGATGAGAGATTGTGTGGGGGGAGTCTTGGGGCTGATAGG 3520
Y G S R Q G V F V R W M R . G D C G G G E S W G .
T M G V G K G C L . G G . D E E I V V G C S L G G D R
L W E . A R G V C K V D E M R R L W W G G V L G V I G
ACCCCTAACAGGATAGATGGCAAACCTGTGTGTGGCAGGCCGTTGTTCCACCCCTTAATTACCGTTGAGGTTGGCAG 3600
D P . Q G . M A N C V W A G R W F H P L N . R . G W Q
T L N R D R W Q T V C G Q A G O S T H L I S V E V G R
P L T G I D G K L C V G R P V V P P T . L A L R L A
GGCTGGAAGGAGCCAGCACTCTCAACCTTGGGAGAAAGTGCAAGTGTGACAGAAGAAGACAGAAAGAGGAGACACCCGGC 3680
G W K E P A L S T L E K V Q V . Q E E T E R G D T R A
A G R S Q H S O P W R K K C K C D K K K K K E E T P G
G L E G A S T L N L G E S A S V T R R N R K R R H P G
AGGGAGCTCCTTGGCATCGTTTCTTCCATGGCCCTGGCTTTGGGAAGAATTAGGAAGGGTGGTGACTCTGCATCCTCA 3760
G S S L P S F L P M A L A L G R I R K G W . L C I L
Q G A P C H R F P P W L W E E L G K G G D S A S
R E L L A I V S S H G P G F G K N . E R V V T L H P Q
GAAAAGCCCTCTCTCCCTCTTGGACTCTGAGGCTTAGAGAGGAGAATGTGTAGGAGGAATGATGTGGAAGAGTAAC 3840
R K A L S P S L D S R G L E R R M C R R N D V E R V T
E K P S L P L W T L E A . R G E C V G G H M W K E . L
K S P L S L F G L S R L R E E N V . E E . C G K S N
TGACCTATCCAGATGTGTCTGTCAATGAGATTTCAGGAATGAGAATGGAATACAGCTGTGCTTACGATGGCCGAGGCC 3920
P I Q M C L . M R F O R . E W K Y S C A S A W P R A
D L S R C V C E . D P R N E N G N T A V L Q H G R G
L T V P D V S V N E I S O M R M E I Q L C F S M A E G
CTTAGGATCCCTCAGCCCCACCCACAGGAAGGAATCATCCAATCATCCACCTGGGGTCTGAGGACATGACATTGAC 4000
L G S L T P T P O E E N H P I I P P G V L R T . H .
P . D P S P P P H R K R I I Q S S H L G F . G H D I D
L R I P H P H P T G R E S S N H P T W G S E D M T L T
ACAGAGCAGGAGAGCTGAGATAGAAACACTCCCTCCTGTCTGTCTCCCACTAAGCCTCACCAGTCTTATTAACTGAT 4080
H R A G E L R . K H S L L S C L P L S L T S P S L T D
T E Q E S . D R N T P S C L V S H . A S P V L H . L I
Q S R R A E I E T L P P V L S P T K P H O S F I N .

FIGURE 15c

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TTGGTGGATGCTAATTATGATGCTCACCCTCAGGTCTCTGCTCCCCCTTTAATCTGGATGAACACCACCACGACTCTTC 4160
W.W.M.L.I.M.I.L.T.P.Q.V.S.A.P.P.L.I.W.M.N.T.T.H.D.S.S
L.V.D.A.N.Y.D.P.H.P.S.G.L.C.S.P.F.N.L.D.E.M.H.P.R.L.F
ACAGGGCCACCAGAGCCGAATTTGGATACAGTGTCTTACAGCATGTTGGGGTGGACAGCATGGTGAGAGGGGAACA 4240
Q.G.H.Q.R.P.N.L.D.T.V.S.Y.S.H.L.G.V.D.S.D.G.R.R.R.N
H.R.A.T.R.G.R.I.W.I.O.C.L.T.A.C.W.Q.W.T.A.M.V.R.O.K.T
T.G.P.P.E.A.E.F.G.Y.S.V.L.Q.H.V.G.G.G.O.R.W.E.G.K.Q
GAGGACCGTGGGATCGGACTATGCACTCACTGATAAAGGGGAGGACCGGTCCAAGCTGGCCCTTTGAAAGTGCCTGGGCG 4320
R.G.P.W.D.R.D.Y.A.L.T.D.K.G.R.D.R.S.K.L.A.F.R.S.A.W.G
E.D.R.G.I.G.T.M.H.S.L.I.K.G.R.T.G.P.S.W.P.L.K.V.P.G.A
R.T.V.G.S.O.L.C.T.H.R.G.G.P.V.Q.A.O.L.K.C.L.G
TCCATGACGTCTCATGCACTCTCCCTCTCACTATACTAAGGACCATGCTCACCAGGATCTTATATCCATATTCTCCTTCC 4400
S.M.T.S.H.A.L.S.L.S.L.V.G.P.C.S.P.D.L.Y.I.H.I.L.L.P
P.R.L.M.H.S.P.S.H.Y.T.K.D.H.A.H.R.I.F.I.S.I.F.S.P
L.H.D.V.S.C.T.L.P.L.T.I.L.R.T.M.L.T.G.S.L.V.P.Y.S.P.S
AGGATGCTGGTGGGCTGCCCTGGGATGGGCCATCAAGTGACCGGAGAGGGATGTTTATCGTTGCTCTATAGGGGGATT 4480
G.C.W.W.V.P.P.G.M.G.H.O.V.T.G.E.G.M.F.I.V.A.L.G.D
Q.D.A.O.G.C.P.L.G.W.A.I.R.P.E.R.G.C.L.S.L.L.L.Y.R.G.I
R.M.L.V.G.A.P.W.D.G.F.S.G.D.R.R.G.D.V.V.R.C.S.I.G.G.F
CCACAGTGTCTCATGTACCAAGGCCACCTGGGTAAGAAGAAGCTGACCTTCCCCCTGCTAATTCCTGATGTTGACATC 4560
S.T.V.L.H.V.P.K.A.T.W.V.R.R.S.L.T.F.P.L.L.I.P.D.V.D.I
P.Q.C.S.H.Y.C.R.P.P.P.G.E.E.A.P.F.F.P.C.F.L.M.L.T.S
H.S.A.P.C.T.K.G.H.L.G.K.K.K.F.D.L.S.P.A.N.S.C.H
TAGTAATCTGACCCCTTGGACCTTGTCTTCAATGACCTGAACCTAAGAAGCCGAACCTATGACCCCATGACTTCATTCT 4640
S.L.P.L.G.P.C.L.G.P.T.K.E.A.E.L.P.H.D.F.I.L
L.S.N.S.D.P.L.D.L.V.F.N.D.P.E.L.K.K.F.N.Y.D.F.M.T.S
L.V.T.L.T.P.W.T.L.S.S.M.T.L.N.R.S.R.T.M.T.P.L.H.S
CTTGACCTTCTCTCAAGCAGGTGACTATCAACTTGGAAATTCCTCTCAGCTGCTGTAATATGCACTAGGATGTC 4720
F.Y.P.S.N.Q.V.T.I.N.L.E.I.P.L.S.L.L.I.C.T.G.C
S.S.T.L.P.P.T.R.L.S.T.W.K.F.L.S.A.C.C.E.Y.A.P.R.D.V
L.L.P.F.L.O.P.G.D.Y.O.L.O.N.S.S.Q.P.A.V.N.M.H.L.G.M.S
TCTACTAGAGACAGATGCTGATGGGGATTTCAGTGGAGCTGAAGAAGGGCTCAGAAGGTTTACAGCAGGGAAGAGAG 4800
L.Y.R.Q.M.L.M.G.D.S.W.A.E.R.R.A.S.E.G.S.O.O.G.R.E
S.T.R.D.R.C.W.G.I.H.G.E.L.K.E.G.P.O.K.V.H.S.R.E.S
L.L.E.T.D.A.D.G.G.G.F.M.V.S.K.K.G.L.R.A.F.T.A.G.K.R
CATATGGTATCTGGGCACTGGTGGCTTGGGCTTTCATCCAGTGTCTCGAGGCGAGTCAAGGCTGATCTACAGAGT 4880
H.Y.G.I.W.A.V.A.W.A.F.H.P.S.V.L.E.A.E.S.G.L.I.Y.R.V
A.L.M.V.S.G.Q.W.W.L.G.P.F.I.P.V.F.W.R.O.S.O.A.S.T.E
GAGTCCAGGACAGCCAGGCTATGCAGAGAAACCTGTTTGAACAAACCAAACTAACCACCAACCAAC 4960
S.S.R.T.A.K.A.M.O.R.N.P.V.L.K.N.P.K.P.K.L.T.K.Q.Q.Q
E.L.Q.D.S.Q.G.Y.A.E.K.P.C.F.E.K.P.K.T.N.Q.T.T.T.T
AGAAAAGCAGCCTGTAGGGAATTAGTCTGTATAGAAGAGACAGGAATTCAAAACCTAGAGAGCAAGGCAAGGTT 5040
Q.K.K.H.R.G.K.G.N.S.V.K.R.Q.G.I.O.N.P.R.E.O.G.R.V
R.K.S.T.V.V.R.E.I.S.L.Y.R.R.D.K.E.F.K.T.L.E.S.K.A.G.F
E.K.A.P.W.G.K.L.V.C.I.E.E.T.R.N.S.K.F.R.A.R.Q.G
CCCCATGAGTGGTCTCCATCTCTCTTTAACTAGGTGTGTGTTCCGAGAGGCCCTCTCAAGCCTGGGGATAACTATTTC 5120
P.H.G.V.V.S.I.S.L.L.T.R.C.V.F.R.E.A.L.S.S.L.G.I.T.I.S
P.M.E.W.S.P.S.L.F.L.G.V.C.S.R.R.P.S.Q.A.W.G.L.F
S.P.W.S.G.L.H.L.S.P.N.V.C.V.P.R.O.P.L.K.P.G.D.N.Y.F
TCCTATCCACCCAGGCTGTGCCCTCTTTGGTCTGGTGCCTGCGCAGCTCTGTCTTCACTTCTGGAATATGIGCCCGT 5200
P.I.H.P.G.L.C.P.S.L.V.S.C.L.R.O.L.C.L.O.F.W.N.M.C.P
L.L.S.T.Q.A.C.A.P.L.W.S.R.A.C.G.S.S.V.F.S.S.G.I.C.A.R
S.Y.P.P.R.P.V.P.L.F.G.L.V.P.A.A.A.L.S.S.V.L.E.Y.V.P.V
GTGGATGCTTCATTCCGGCCCCAGGGAAGCCTGGCACCCACCGCCCAACGTGAGCCAGTGGAAAGGGCCCTGGAAAGCTCAG 5280
C.G.C.F.I.P.A.P.O.G.K.P.G.T.H.R.P.T.A.S.C.R.A.L.E.A.O
V.D.A.S.F.R.P.O.G.S.L.A.P.T.A.O.R.E.P.V.E.G.P.W.K.L.S
W.M.L.H.S.G.P.R.E.A.W.H.P.F.P.N.V.S.Q.W.K.G.P.G.S.S
TTCCAGATAGGATGCTGGGTGGGAAACTAGGACAAAGACTTGGTGGAGGGTCTGCATGGCTATCCTCATCTCC 5360
F.P.D.R.D.A.G.W.E.K.L.G.Q.R.L.G.G.G.S.A.W.L.S.S.S.F.P
V.S.Q.I.G.M.L.G.G.K.N.D.K.D.L.V.E.G.L.H.G.Y.P.H.S
V.P.R.G.C.W.V.G.K.T.R.K.T.W.W.R.V.C.M.A.I.L.I.I.P
AAGTGTGCTGTCAGAGAGGCTCTGTTTCTAAGTATTAGAACTCAGACTCCTTAGCAGAGCCTCAAGACACCAGGAT 5440
S.V.L.A.E.E.A.P.V.C.L.I.R.I.Q.T.P.E.S.L.K.T.P.O
Q.V.C.L.Q.K.R.L.L.P.A.N.L.S.F.R.L.L.R.A.A.S.R.H.O
K.C.A.C.R.R.G.S.C.L.L.T.D.N.S.D.S.L.G.E.P.Q.D.T.R.I

FIGURE 15d

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CTGGTTTACCAACTTAAAAACAAAACAAAACAGCATATCCTGTGCACAGCCTATCCCTCATCCATCAGGTGTCCTCCAT 5520
S G F T N L K T K Q N S I S C A Q P I P H P S R V L H
L V L P T . K Q N K T A Y P V H S L S L I H H V S S I
W F Y Q L K N K T K Q H I L C T A Y P S S I T C P P
ATCTTATTTTGTGGTCTTATAGATGCCAAGTCAGCACTCAGTTATTGGGTTCTCCCTCATGCCCTTTCATATCTTC 5600
I L F L W V L . M P S Q H S V I G F S P H A F H I L S
S Y F C G S Y R C Q V S T Q L L G S P L M . P F I Y F
Y L I F V G L I D A K S A L S Y W V L F S C L S Y T F
TTATCTACTGCCCTTTGGGAGATAGTCTTATGTAGCCAGGCTGTCTGTGATCTTGAATTTCCTTGCCTCAGCTTCTCA 5680
Y L L P P G R . S Y V A Q A V L D L G I C L P Q L L
L I Y C L L O D S L H . P R L S L I L E F A C L S F S
L S T A F W S I V L C S F G C P . S W N L L A S A S Q
GTCTCAAGTACTGGGATAATAGGCATGCTGTCTGCCCTGGCTTTGCTGAACATGCCCTCTGTGGCCATTGGTAGGCCA 5760
S L K Y W D N R H A L S A W P L L N M P S V A I G R A
V S S T G I I G M H C L P G L C . T C P L W P L V G H
S Q V L G . . A C I V C L A F A E H A L C G H W . G
TGAGTCAAACTACTGCCCTCCGCCACACACACACAAAGTGAAGGCTCTCTAAGTGTCCATAGCACAGGGTACT 5840
. V K Y C P P P Q H T H K R K . G S L S V P . H R V V
E S N T A L P H N T H T H E S E A L . V F H S T G .
H S O I L P S P T T H T Q T K V R L S K C S I A Q O S
GGTAGGCCCTCTGGTAGTGATATTTCTTTTACTCTGCCCATCTCTTCTTTCTTTGATTTCACACTGGGGACCTG 5920
V G L S L V H I S F F Y S A H L F F L . F P H W G F
W . A S R . C I F H S F T L P I S S F F D F H T G D L
G R P L A S A Y F I L L L C P S L L S L I S T L G T W
GCATAGTACTTTCTGTAAATTAGAGAGAATTCCTTTTAAAGTGCCTGCATTGCAGGCTCCTCTGGACATTCTCCCT 6000
G I V L S W . L R E N S L L S A C I A A S S W D I L P
A . Y F P G N . E R I P F . V P A L Q R P P G T F S L
H S T F L V I K R E F P F K C L H G S V L L G H S F
TGCTGACTACACCCGACATCCTTCGATGTTTTTGTTCCTCATCACTATGCCGCCCTTCTAGGCTGTCCACATACATG 6080
C . L H F T S F H V F C F P S L C P P S R L S H I K G
A D Y T P H P S M F F V S H H Y A P L L G C P T Y M
L L T T P H I L P C F L F P I T M P P F . A V P H T W
ATGCTGCTATTGTTTTGGATGGCTCCACAGTATCTATCCCTGGTCAAGTTCAGACTTTCCTTGGAGGCTGTAGGA 6160
C R H C F G W L Q Q Y L S L V R S S D F P S E A G R
D V V I V L D G S N S I Y P W S E V O T F L R R L V G
N S S L P W H A P T V S Y P G Q K F R L S F G G W . E
AGACTGTTTCATCGATCCGGAGGAGATACAGGTAAAGAGAAGATATGCGATAGGATTCGAGGCAAGAAAGTAAACACTCC 6240
K T V H R S G A D T G K R K I C G . D W R E R S K H S
R L F I D P E O I Q V R E R Y V D R I G G K E V N T P
D C S S I R S R Y R . E K D M W I G L E G K K . T L
TGGACCCCTGGATGTAAGCAGCCATGTCAGGCTCTTGATGACACCCCTGGGACATTGTCTTCTACAGAACTCATGCTCAA 6320
W T L G C K Q P C P A S . . H P G T L S S T E L M L K
G P L D V S S H V Q P L D D T L G H C L L O N S L K
L D P W M . A A H S S L L M T P W D I V F Y R T H A Q
GAAGTGTGCAATTAACTTACCAAAAAGTCACAAAATTTTATAATGTTTGAAGTAAGTTTATGATTGTGTGGGGGCCAC 6400
N C A I N L P K S H K N F I H F E V S L . L C G G P
R T V Q L T Y O K V T K I S . C L K . V Y D C V G G H
E L C N . L T K K S O K F H N V . S K F H I V W G A T
ACTGAGAGCTTCCCTTTGCTGCTTGTATGCTTGGGCAATGCATGCCATGAGCTGCAAGTTAGACACAGCTGTTCACTT 6480
H S E L P F A A C S C L G N A C H E L Q V R H T C S L
T O S P P L L L V V A W A M H A M S C K L D T P V H F
L R A S L C C L . L L G Q C M P . A A S . T H L F T
CCCTTCATCGTGTGCAGGTTGGACACAGCTGTTAGGGGTTCACTTCCTTCATCTTTGTGCTCATCTTCTCTAG 6560
P L H R A A G W T H L L G V H F P P I L C A P S S L R
P F I V L O V G H T C . G P T S P S S F V L H L L Y
S P S S C R L D T P V R O S L F L H F L C S I F S T
CTCTTCATACATCCCATGTGGGCACATGCTTATGTTCTCAGGTAGGACTGGTACAGTACGGGGAGAACCTGTGTCATG 6640
S S Y I P C G H M V Y C S Q V G L V Q Y G E N P V H
A L H T S H V G T W S I V L R . D W Y S T G R T L C M
L F I H P M W A H G L L F S G R T G T V R G E P C A
AGTGTCCCTGGGAGACTTCCGAACAAAGGAAGAAGTGTGAGAGCAGCAAGGAACCTAAGTCCGAGGGAAGGGCGAGAA 6720
E W S L G D F R T K E E V V R A A R N L S R R E G R E
S G P W E T S S R K K L . E Q U G T . V G G G K G R E
V V P G R L P N K G R S C E S S K E P K S E G R A R
ACGAGAACCGCCCAAGGATCATGCTGGCATGCTGAGACATTGTAAAGCGGCTGTGTGAGGAGGAGGAAGGATCAGCAG 6800
T R T A O A I M V A W . D I V K G S C E G G G R I S R
R E P P K R S W W H G E T L . A G R V R E E E G S A
N E N R P S D H G G M V R H C K G V V . G R R K D O Q

FIGURE 15e

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[illegible]

FIGURE 15f



FIGURE 16

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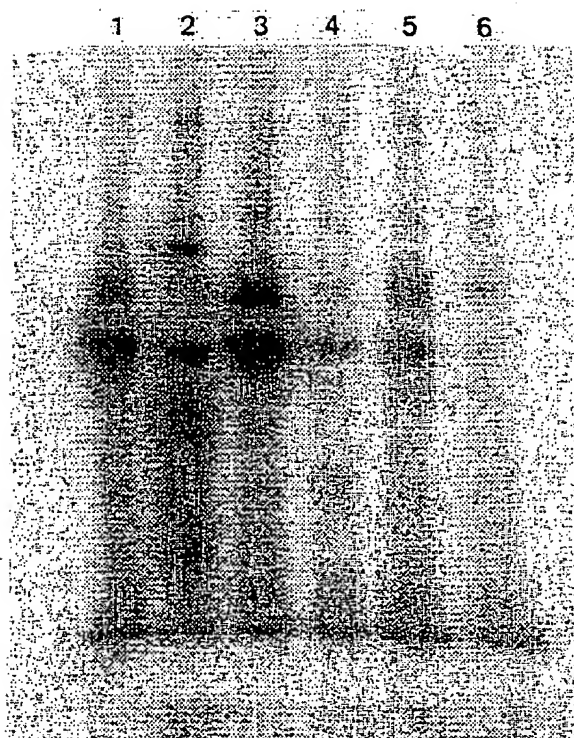


FIGURE 17

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